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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C07K 7/04, 14/025, 14/16, C12N 9/94, 9/96, 9/98, 9/99	A1	(11) International Publication Number: WO 96/19495 (43) International Publication Date: 27 June 1996 (27.06.96)
(21) International Application Number: PCT/US95/16733 (22) International Filing Date: 20 December 1995 (20.12.95) (30) Priority Data: 360,107 20 December 1994 (20.12.94) US 470,896 6 June 1995 (06.06.95) US (71) Applicants: DUKE UNIVERSITY [US/US]; Erwin Road, Durham, NC 27706 (US). TRIMERIS INC. [US/US]; 4727 University Drive, Durham, NC 27707-3438 (US). (72) Inventors: BOLOGNESI, Dani, P.; 17 Harvey Place, Durham, NC 27705 (US). MATTHEWS, Thomas, J.; 5906 Newhall Road, Durham, NC 27713 (US). WILD, Cart, T.; 1702 B Vista Street, Durham, NC 27701 (US). BARNEY, Shawn, O'Lin; 106 Branchway Road, Cary, NC 27502 (US). LAMBERT, Dennis, M.; 101 Centerville Court, Cary, NC 27513 (US). PETTEWAY, Stephen, R., Jr.; 203 Le Gault Drive, Cary, NC 27513 (US). LANGLOIS, Alphonse, J.; 1720 Vista Street, Durham, NC 27701 (US). (74) Agents: CORUZZI, Laura, A. et al.; Pennie & Edmonds, 1155 Avenue of the Americas, New York, NY 10036 (US).		(81) Designated States: AL, AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LS, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, LS, MW, SD, SZ, UG). Published <i>With international search report.</i>
(54) Title: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION (57) Abstract The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID: 1) peptide corresponding to amino acids 638 to 673 of the HIV-1 LAI gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.		

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**METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION**

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a
5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government
10 support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

1. INTRODUCTION

15 The present invention relates, first, to DP178 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1_{LAI} transmembrane protein (TM) gp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability,
20 antiviral activity, such as the ability to inhibit HIV transmission to uninfected CD-4⁺ cells, or an ability to modulate intracellular processes involving coiled-coil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178
25 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. The present invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids
30 558 to 595 of the HIV-1_{LAI} transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion
35 capability, antiviral activity, or the ability to

modulat intracellular processes inv lving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, non-cytotoxic inhibitors of HIV-1 transfer to uninfected CD-4⁺ cells. The invention is further demonstrated by Examples wherein peptides having structural and/or amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral activity.

2. BACKGROUND OF THE INVENTION

2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.

Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

5 Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell
10 death.

2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly
15 degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo, R. et al., 1984, Science 224:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science 233:343-346; Guyader, M. et al., 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of
20 each of these types. Infection of human CD-4⁺ T-lymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.

25 HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and
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replicate via a DNA intermediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, Science 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell leukemia viruses (HTLV-I, -II, -III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral RNA genome and those enzymes required for early replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped surface glycoproteins are synthesized as a single 160 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, gp41 and gp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains non-covalently associated with gp41, possibly in a trimeric or multimeric form (Hammarskjold, M. and Rekosh, D., 1989, Biochem. Biophys. Acta 989:269-280).

HIV is targeted to CD-4⁺ cells because the CD-4 cell surface protein acts as the cellular receptor for the HIV-1 virus (Dalglish, A. et al., 1984, Nature 312:763-767; Klatzmann et al., 1984, Nature 312:767-768; Maddon et al., 1986, Cell 47:333-348). Viral entry into cells is dependent upon gp120 binding the cellular CD-4⁺ receptor molecules (McDougal, J.S. et al., 1986, Science 231:382-385; Maddon, P.J. et al., 1986, Cell 47:333-348) and thus explains HIV's tropism for CD-4⁺ cells, while gp41 anchors the enveloped glycoprotein complex in the viral membrane.

2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the
5 successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991,
10 FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptase-targeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been
15 developed which have been shown to be active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989,
20 Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

Attempts are also being made to develop drugs
25 which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4⁺ T-cells by some
30 HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,
35

recombinant soluble CD-4 clinical trials have produced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

5 The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and
10 drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

15 Attention is also being given to the development of vaccines for the treatment of HIV infection. The HIV-1 enveloped proteins (gp160, gp120, gp41) have been shown to be the major antigens for anti-HIV antibodies present in AIDS patients (Barin, et al., 1985, Science 228:1094-1096). Thus far, therefore,
20 these proteins seem to be the most promising candidates to act as antigens for anti-HIV vaccine development. To this end, several groups have begun to use various portions of gp160, gp120, and/or gp41 as immunogenic targets for the host immune system.
25 See for example, Ivanoff, L. et al., U.S. Pat. No. 5,141,867; Saith, G. et al., WO 92/22,654; Shafferman, A., WO 91/09,872; Formoso, C. et al., WO 90/07,119. Clinical results concerning these candidate vaccines, however, still remain far in the future.

30 Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

35

3. SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate LAI (HIV-1_{LAI}), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1_{LAI}, but found in viruses and/or organisms other than HIV-1_{LAI}. Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1_{LAI}, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178-like amino acid sequences present in nonviral organisms.

The invention further relates to peptides DP107 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1_{LAI} transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the

DP107 peptide sequence present within the gp41 protein of HIV-1_{LAI}, but found in viruses and organisms other than HIV-1_{LAI}. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1_{LAI}, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4⁺ cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides.

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-associated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that

th peptides of the invention may be used as modulators of intracellular events involving coiled-coil peptide structures.

The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. The term "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.

Embodiments of the invention are demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4⁺ cell-cell fusion (*i.e.*,
5 syncytial formation) and infection of CD-4⁺ cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

10 The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery
15 is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and
20 DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein
25 peptides, from a variety of viral and nonviral sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are presented wherein a number of the peptides of the
30 invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.

3.1. DEFINITIONS

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with
5 respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino
10 acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as
15 follows:

A (alanine)
R (arginine)
N (asparagine)
D (aspartic acid)
C (cysteine)
20 Q (glutamine)
E (glutamic acid)
G (glycine)
H (histidine)
I (isoleucine)
L (leucine)
K (lysine)
M (methionine)
25 F (phenylalanine)
P (proline)
S (serine)
T (threonine)
W (tryptophan)
Y (tyrosine)
V (valine)

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4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Amino acid sequence of DP178 (SEQ ID:1) derived from HIV_{LAJ}; DP178 homologs derived from HIV-1_{SP2} (DP-185; SEQ ID:3), HIV-1_{RF} (SEQ ID:4), and HIV-1_{MOJ} (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2_{red} (SEQ ID:6) and HIV-2_{NDZ} (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which inhibits HIV-1 cell free virus infection; DP-125 (SEQ ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. Throughout the figures, the one letter amino acid code is used.

FIG. 2. Inhibition of HIV-1 cell-free virus infection by synthetic peptides. IC₅₀ refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 3. Inhibition of HIV-1 and HIV-2 cell-free virus infection by the synthetic peptide DP178 (SEQ ID:1). IC₅₀: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.

4B: DP-180 (SEQ ID:2) represents a scrambled control peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1_{SP2} isolate; Control, refers to the number of syncytial produced in the absence of peptide.

5 FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.

 FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1) and DP-116 (SEQ ID:9) on CEM cells. Cell
10 proliferation data is shown.

 FIG. 7. Schematic representation of HIV-gp41 and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter
15 P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM.
20 The proteins are more fully described, below, in Section 8.1.1.

 FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.

 FIG. 9. Abrogation of DP178 anti-HIV activity.
25 Cell fusion assays were carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41PΔ178.

 FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.

30 FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common
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features of both models include (1) the native state is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally through gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other. In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended α -helix. This conformational change positions the fusion peptide for interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be

the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

5 FIG. 18. Hybrid motif design ALLMOTI5 crossing GCN4, DP107, DP178, c-Fos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

10 FIG. 20. Search results for HIV-1 (BRU isolate) enveloped protein gp41. Sequence search motif designations: Spades (♠): 107x178x4; Hearts (♥) ALLMOTI5; Clubs (♣): PLZIP; Diamonds (♦): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program
15 designed to search for such peptide regions). Asterisk (*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences chosen based on 107x178x4 searches are underlined and
20 in bold. DP107 and DP178 sequences are marked, and additionally double-underlined and italicized.

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations
25 are as in FIG. 20.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations
30 are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations
35 are as in FIG. 20.

FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

5 FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

10 FIG. 26. Search results for influenza A virus (strain A/AICHI/2/68) hemagglutinin precursor HA2. Sequence search designations are as in FIG. 20.

FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data. FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D: 15 Peptides derived from the F1 DP107-like region. Peptide and CD data.

Antiviral activity (AV) is represented by the following qualitative symbols:

20 "-", negative antiviral activity;
 "+/-", antiviral activity at greater than 100µg/ml;
 "+", antiviral activity at between 50-100µg/ml;
 "++", antiviral activity at between 20-50µg/ml;
 "+++", antiviral activity at between 1-20µg/ml;
25 "++++", antiviral activity at <1µg/ml.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

30 "-", no helicity;
 "+", 25-50% helicity;
 "++", 50-75% helicity;
 "+++" 75-100% helicity.

IC₅₀ refers to the concentration of peptide necessary to produce only 50% of the number of syncytial relative to infected control cultures 35

c ntaining no peptide. IC_{50} values were obtained using purified peptides only.

FIG. 28A-B. Respiratory Syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. IC_{50} values were obtained using purified peptides only.

FIG. 29A-B. Peptides derived from the HPIV3 F1 DP107-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. Purified peptides were used to obtain IC_{50} values, except where the values are marked by an asterisk (*), in which cases, the IC_{50} values were obtained using a crude peptide preparation.

FIG. 30A-B. Peptides derived from the HPIV3 F1 DP178-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. Purified peptides were used to obtain IC_{50} values, except where the values are marked by an asterisk (*), in which cases, the IC_{50} values were obtained using a crude peptide preparation.

FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as in FIG. 20.

FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

FIG. 33. Motif search results for Epstein-Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "@" refers to a well known DNA binding domain and "+" refers to a well known dim rization domain, as defined

by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

5 FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

10 FIG. 36. Motif search results for simian Mason-Pfizer monkey virus, enveloped (TM) protein gp20. Sequence search designations are as in FIG. 20.

FIG. 37. Motif search results for *Pseudomonas aeruginosa*, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

15 FIG. 38. Motif search results for *Neisseria gonorrhoeae* fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 39. Motif search results for *Hemophilus influenzae* fimbrial protein. Sequence search designations are as in FIG. 20.

20 FIG. 40. Motif search results for *Staphylococcus aureus*, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

25 FIG. 41. Motif search results for *Staphylococcus aureus* enterotoxin Type E. Sequence search designations are as in FIG. 20.

FIG. 42. Motif search results for *Staphylococcus aureus* enterotoxin A. Sequence search designations are as in FIG. 20.

30 FIG. 43. Motif search results for *Escherichia coli*, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 44. Motif search results for human c-fos proto-oncoprotein. Sequence search designations are as in FIG. 20.

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FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

5 FIG. 46. Motif search results for human zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. IC_{50} values were obtained using purified peptides.

10 FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D "NT", not tested.

15 FIG. 49A-C. DP178-derived peptide antiviral data. The peptides listed herein were derived from the region surrounding the HIV-1 BRU isolate DP178 region (e.g., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point mutations, the mutated amino acid residues are shown with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amido- and acetyl- blocking groups found on such peptides), such modifications are indicated. FIG. 49A: The column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one amino acid peptide "walk" across the DP178 region. The next column to the right indicates whether the test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B: The column to the immediate right of the test peptide name

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indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself. IC_{50} is as defined in FIG. 27A-D, and IC_{50} values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC_{50} was obtained using a crude peptide preparation.

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data. IC_{50} as defined in FIG. 27A-D, and IC_{50} values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC_{50} was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide. The

length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

FIG. 52A-B. Hepatitis B virus subtype AYW major surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

5. DETAILED DESCRIPTION OF THE INVENTION

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1_{LAI} transmembrane (TM) gp41 protein. Such DP107 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate

intracellular processes involving coil d-coil structures.

Further, peptides of the invention include DP107 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the peptides of the invention. Further, procedures are described for the use of the peptides of the invention for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the following model is proposed to explain the potent anti-HIV activity of DP178, based, in part, on the experiments described in the Examples, infra. In the HIV protein, gp41, DP178 corresponds to a putative α -helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal site on gp41 whose interactive structure is influenced by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. It is of interest that mutations in the C-terminal α -helix motif of gp41 (i.e., the D178 domain) tend to enhance the fusion ability of gp41, whereas mutations in the leucine zipper region (i.e., the DP107 domain) decrease or abolish the fusion ability of the viral protein. It may be that the leucine zipper motif is involved in membrane fusion while the C-terminal α -helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virus-induced membrane fusion.

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On the basis of the foregoing, two models are proposed of gp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for gp41 - one in a "native" state as it might be found on a resting virion. The other in a "fusogenic" state to reflect conformational changes triggered following binding of gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. FIG. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B can be considered.

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107

peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, *infra*, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178 domains (excluding the fusion peptide, transmembrane region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides -- the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. This transformation may result from liberation of the potent DP178 domain from a molecular clasp with the leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

5.1. DP178 AND DP178-LIKE PEPTIDES

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1_{LA1} isolate, and has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH₂-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:1)

In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. Truncations of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below.

Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group ($-NH_2$) and "Z" may represent a carboxyl ($-COOH$) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE I
DP178 (SEQ ID:1) CARBOXY TRUNCATIONS

X-YTS-Z
 X-YTSL-Z
 X-YTSLI-Z
 X-YTSLIH-Z
 5 X-YTSLIHS-Z
 X-YTSLIHSL-Z
 X-YTSLIHSLI-Z
 X-YTSLIHSLIE-Z
 X-YTSLIHSLIEE-Z
 X-YTSLIHSLIEES-Z
 X-YTSLIHSLIEESQ-Z
 10 X-YTSLIHSLIEESQN-Z
 X-YTSLIHSLIEESQNNQ-Z
 X-YTSLIHSLIEESQNNQQ-Z
 X-YTSLIHSLIEESQNNQQE-Z
 X-YTSLIHSLIEESQNNQQEK-Z
 X-YTSLIHSLIEESQNNQQEKN-Z
 X-YTSLIHSLIEESQNNQQEKNE-Z
 X-YTSLIHSLIEESQNNQQEKNEQ-Z
 15 X-YTSLIHSLIEESQNNQQEKNEQE-Z
 X-YTSLIHSLIEESQNNQQEKNEQEEL-Z
 X-YTSLIHSLIEESQNNQQEKNEQEELL-Z
 X-YTSLIHSLIEESQNNQQEKNEQEELLE-Z
 X-YTSLIHSLIEESQNNQQEKNEQEELLEL-Z
 X-YTSLIHSLIEESQNNQQEKNEQEELLELD-Z
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDK-Z
 20 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKW-Z
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWA-Z
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWL-Z
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWLW-Z
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWLWN-Z
 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWLWNW-Z
 25 X-YTSLIHSLIEESQNNQQEKNEQEELLELDKWLWNWF-Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IA
DP178 (SEQ ID:1) AMINO TRUNCATIONS

	X-NWF-Z
	X-WNWF-Z
	X-LWNWF-Z
5	X-SLWNWF-Z
	X-ASLWNWF-Z
	X-WASLWNWF-Z
	X-KWASLWNWF-Z
	X-DKWASLWNWF-Z
	X-LDKWASLWNWF-Z
	X-ELDKWASLWNWF-Z
10	X-LLELDKWASLWNWF-Z
	X-ELLELDKWASLWNWF-Z
	X-QELLELDKWASLWNWF-Z
	X-EQELLELDKWASLWNWF-Z
	X-NEQELLELDKWASLWNWF-Z
	X-KNEQELLELDKWASLWNWF-Z
	X-EKNEQELLELDKWASLWNWF-Z
15	X-QEKNEQELLELDKWASLWNWF-Z
	X-QQEKNEQELLELDKWASLWNWF-Z
	X-NQQEKNEQELLELDKWASLWNWF-Z
	X-QNQQEKNEQELLELDKWASLWNWF-Z
	X-SQNQQEKNEQELLELDKWASLWNWF-Z
	X-ESQNQQEKNEQELLELDKWASLWNWF-Z
	X-EESQNQQEKNEQELLELDKWASLWNWF-Z
	X-IEESQNQQEKNEQELLELDKWASLWNWF-Z
20	X-LIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-SLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-HSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-IHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-LIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
	X-TSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
25	X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP178-like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing
5 dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The
10 insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that
15 insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178
20 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to
25 modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein
30 regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178
35 region of the gp41 protein.

Deletions of DP178 (SEQ ID:1) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

5.2. DP107 AND DP107-LIKE PEPTIDES

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to residues 558 to 595 of HIV-1_{LAI} transmembrane (TM) gp41 protein, as shown here:

NH₂-NNLLRAIEAQHLLQLTVWQIKQLQARILAVERYLKDQ-COOH
(SEQ ID:25)

In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes

inv lving coiled-c il peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below.

5 Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group ($-NH_2$) and "Z" may represent a carboxyl ($-COOH$) group. Alternatively, "X" may represent a hydrophobic group, including but not
10 limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or
15 peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred
20 "X" or "Z" macromolecular group is a peptide group.

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TABLE II
DP107 (SEQ ID:25) CARBOXY TRUNCATIONS

	X>NNL-Z
	X>NNLL-Z
	X>NNLLR-Z
5	X>NNLLRA-Z
	X>NNLLRAI-Z
	X>NNLLRAIE-Z
	X>NNLLRAIEA-Z
	X>NNLLRAIEAQ-Z
	X>NNLLRAIEAQQ-Z
	X>NNLLRAIEAQQH-Z
10	X>NNLLRAIEAQQHL-Z
	X>NNLLRAIEAQQHLL-Z
	X>NNLLRAIEAQQHLLQ-Z
	X>NNLLRAIEAQQHLLQL-Z
	X>NNLLRAIEAQQHLLQLT-Z
	X>NNLLRAIEAQQHLLQLTV-Z
	X>NNLLRAIEAQQHLLQLTVW-Z
	X>NNLLRAIEAQQHLLQLTVWQ-Z
15	X>NNLLRAIEAQQHLLQLTVWQI-Z
	X>NNLLRAIEAQQHLLQLTVWQIK-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQ-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQL-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQ-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQA-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQAR-Z
20	X>NNLLRAIEAQQHLLQLTVWQIKQLQARI-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVE-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVER-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z
25	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKD-Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-Z

The one letter amino acid code is used.

Additionally,

- 30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.
- 35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IIA
DP178 (SEQ ID:25) AMINO TRUNCATIONS

	X-KDQ-	Z
	X-LKDQ-	Z
5	X-YLKDQ-	Z
	X-RYLKDQ-	Z
	X-ERYLKDQ-	Z
	X-VERYLKDQ-	Z
	X-AVERYLKDQ-	Z
	X-LAVERYLKDQ-	Z
	X-ILAVERYLKDQ-	Z
10	X-RILAVERYLKDQ-	Z
	X-ARILAVERYLKDQ-	Z
	X-QARILAVERYLKDQ-	Z
	X-LQARILAVERYLKDQ-	Z
	X-QLQARILAVERYLKDQ-	Z
	X-KQLQARILAVERYLKDQ-	Z
	X-IKQLQARILAVERYLKDQ-	Z
	X-QIKQLQARILAVERYLKDQ-	Z
15	X-WQIKQLQARILAVERYLKDQ-	Z
	X-VWQIKQLQARILAVERYLKDQ-	Z
	X-TVWQIKQLQARILAVERYLKDQ-	Z
	X-LTVWQIKQLQARILAVERYLKDQ-	Z
	X-QLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LLQLTVWQIKQLQARILAVERYLKDQ-	Z
20	X-HLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-QHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-QQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
25	X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z
	X>NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-	Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the invention also include DP107-like peptides. "DP107-like", as used herein, refers, first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP107-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of the invention. Utilizing the DP107 and DP107 analog sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids of similar charge, size, and/or

hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. The insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107 region of the gp41 protein.

Deletions of DP107 (SEQ ID:25) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

5.3. DP107 and DP178 ANALOGS

Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1_{LAI} enveloped viruses, non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the

ability to modulate intracellular processes involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond to peptide sequences present in non enveloped and non-viral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found, or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (*i.e.*, other than HIV-1_{LAI}) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates. DP178 analogs derived from the corresponding gp41 peptide region of other (*i.e.*, non HIV-1_{LAI}) HIV-1 isolates may include, for example, peptide sequences as shown below.

NH₂-YTNTIYTLLEESQNQQEKNEQEELLELDKWASLWNWF-COOH (DP-185; SEQ ID:3);

NH₂-YTGIIYNLLEESQNQQEKNEQEELLELDKWANLWNWF-COOH (SEQ ID:4);

NH₂-YTSLIYSLLEKSQIQQEKNEQEELLELDKWASLWNWF-COOH (SEQ ID:5).

SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from HIV-1_{SF2}, HIV-1_{RF}, and HIV-1_{MN} isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding position in the DP178 (SEQ ID:1) peptide. One such

DP178 analog, DP-185 (SEQ ID:3), is described in the Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral activity. The DP178 analogs of the invention may also include truncations, as described above. Further, the
5 analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41
10 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178
15 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV-2_{NIH2} isolate has the 36 amino acid
20 sequence (reading from amino to carboxy terminus):

NH₂-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

Table III and Table IV show some possible truncations
25 of the HIV-2_{NIH2} DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right)
30 terminus. "X" may represent an amino group (-NH₂) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-
35 fluorenylmethoxy-carbonyl (Fmoc) group; or a

c valently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached
5 macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE IIIHIV-2_{NDZ} DP178 analog carboxy truncati ns.

X-LEA-Z
 X-LEAN-Z
 X-LEANI-Z
 X-LEANIS-Z
 5 X-LEANISQ-Z
 X-LEANISQS-Z
 X-LEANISQSL-Z
 X-LEANISQSLE-Z
 X-LEANISQSLEQ-Z
 X-LEANISQSLEQA-Z
 X-LEANISQSLEQAAQ-Z
 10 X-LEANISQSLEQAQI-Z
 X-LEANISQSLEQAQIQ-Z
 X-LEANISQSLEQAQIQQ-Z
 X-LEANISQSLEQAQIQQE-Z
 X-LEANISQSLEQAQIQQEK-Z
 X-LEANISQSLEQAQIQQEKN-Z
 X-LEANISQSLEQAQIQQEKNM-Z
 X-LEANISQSLEQAQIQQEKNMY-Z
 15 X-LEANISQSLEQAQIQQEKNMYE-Z
 X-LEANISQSLEQAQIQQEKNMYEL-Z
 X-LEANISQSLEQAQIQQEKNMYELQ-Z
 X-LEANISQSLEQAQIQQEKNMYELQK-Z
 X-LEANISQSLEQAQIQQEKNMYELQKL-Z
 X-LEANISQSLEQAQIQQEKNMYELQKLN-Z
 X-LEANISQSLEQAQIQQEKNMYELQKLNS-Z
 20 X-LEANISQSLEQAQIQQEKNMYELQKLNSW-Z
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWD-Z
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDV-Z
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFT-Z
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTN-Z
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNW-Z
 X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
 25

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or
 30 T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier
 35 group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IV

HIV-2_{NDH2} DP178 analog amino truncations.

	X-NWL-Z
	X-TNWL-Z
	X-FTNWL-Z
5	X-VFTNWL-Z
	X-DVFTNWL-Z
	X-WDVFTNWL-Z
	X-SWDVFTNWL-Z
	X-NSWDVFTNWL-Z
	X-LNSWDVFTNWL-Z
	X-KLNSWDVFTNWL-Z
	X-QKLNSWDVFTNWL-Z
10	X-LQKLNSWDVFTNWL-Z
	X-ELQKLNSWDVFTNWL-Z
	X-YELQKLNSWDVFTNWL-Z
	X-MYELQKLNSWDVFTNWL-Z
	X-NMYELQKLNSWDVFTNWL-Z
	X-KNMYELQKLNSWDVFTNWL-Z
	X-EKNMYELQKLNSWDVFTNWL-Z
15	X-QEKNMYELQKLNSWDVFTNWL-Z
	X-QQEKNMYELQKLNSWDVFTNWL-Z
	X-IQQEKNMYELQKLNSWDVFTNWL-Z
	X-QIQQEKNMYELQKLNSWDVFTNWL-Z
	X-AQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-QAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-EQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-LEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
20	X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-QSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-ANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
	X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
25	X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

DP178 and DP107 analogs are recognized or identified, for example, by utilizing one or more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

The search strategies are described fully, below, in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV). Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or otherwise, based on primary sequence homology, alone.

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et al., 1991 Science 252:1162-1164) is inadequate for

identifying protein regions analog us to DP107 r
DP178.

Specifically, analysis of HIV-1 gp160 (containing both gp120 and gp41) using the Lupas algorithm does not identify the coiled-coil region within DP107. It
5 does, however, identify a region within DP178 beginning eight amino acids N-terminal to the start of DP178 and ending eight amino acids from the C-terminus. The DP107 peptide has been shown
10 experimentally to form a stable coiled coil. A search based on the Lupas search algorithm, therefore, would not have identified the DP107 coiled-coil region. Conversely, the Lupas algorithm identified the DP178 region as a potential coiled-coil motif. However, the
15 peptide derived from the DP178 region failed to form a coiled coil in solution.

A possible explanation for the inability of the Lupas search algorithm to accurately identify coiled-coil sequences within the HIV-1 TM, is that the Lupas algorithm is based on the structure of coiled coils
20 from proteins that are not structurally or functionally similar to the TM proteins of viruses, antiviral peptides (e.g. DP107 and DP178) of which are an object of this invention.

The computer search strategy of the invention, as
25 demonstrated in the Examples presented below, in Sections 9 through 16 and 19 through 25, successfully identifies regions of proteins similar to DP107 or DP178. This search strategy was designed to be used with a commercially-available sequence database
30 package, preferably PC/Gene.

A series of search motifs, the 107x178x4, ALLMOTI5 and PLZIP motifs, were designed and engineered to range in stringency from strict to broad, as discussed in this Section and in Section 9,
35 with 107x178x4 being preferred. The sequences

identified via such search motifs, such as those listed in Tables V-XIV, below, potentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by brackets, i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed or braced amino acids is followed by a number in parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g., a (2) means "for the next two heptad amino acid positions".

The ALLMOTI5 is written as follows:

```
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
{CDGHP}-{CFP}(2)-{CDGHP}-{CFP}(3)-
```

Translating this motif, it would read: "at the first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, or P is acceptable, at the fourth heptad position (D), any amino acid residue except C,

D, G, H, or P is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTI5 motif, a 35-mer search is preferred. Those viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino acid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-
 [EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is designed to search for

four consecutive heptad repeats (thus the repeat of
th first line four times), meaning that it search s
for 28-mer sized peptides. It may also be designed to
search for 35-mers, by repeating the initial motif
five times. With respect to the 107x178x4 motif, a
5 28-mer search is preferred.

Those viral (non-bacteriophage) sequences
identified via such a 107x178x4 motif are listed in
Table VI, below, at the end of this Section, with
those viral (non-bacteriophage) sequences listed in
10 Table VII, below at the end of this Section, being
preferred.

The 107x178x4 search motif was also utilized to
identify non-viral procaryotic protein sequences, as
listed in Table VIII, below, at the end of this
15 Section. Further, this search motif was used to
reveal a number of human proteins. The results of
this human protein 107x178x4 search is listed in Table
IX, below, at the end of this Section. The sequences
listed in Tables VIII and IX, therefore, reveal
20 peptides which may be useful as antifusogenic
compounds or in the identification of antifusogenic
compounds, and are intended to be within the scope of
the invention.

The PLZIP series of motifs are as listed in FIG.
25 19. These motifs are designed to identify leucine
zipper coiled-coil like heptads wherein at least one
proline residue is present at some predefined distance
N-terminal to the repeat. These PLZIP motifs find
regions of proteins with similarities to HIV-1 DP178
30 generally located just N-terminal to the transmembrane
anchor. These motifs may be translated according to
the same convention described above. Each line
depicted in FIG. 19 represents a single, complete
search motif. "X" in these motifs refers to any amino
35 acid residue. In instances wherein a motif contains

two numbers within parentheses, this refers to a variable number of amino acid residues. For example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive, may be any amino acid".

5 Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP, P1CTLZIP and P2CTLZIP search motifs, Table XI lists
10 viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII lists viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral sequences identified via P12LZIPC searches and Table
15 XIV lists viral sequences identified via P23TLZIPC search motifs. The viral sequences listed in these tables represent peptides which potentially exhibit antiviral activity, may be useful in the identification of antiviral compounds, and are
20 intended to be within the scope of the invention.

 The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify
25 substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-
30 measles virus activity and the Example presented in Section 27 describes peptides with anti-simian immunodeficiency virus activity.

 The DP107 and DP178 analogs may, further, contain any of the additional groups described for DP178,
35 above, in Section 5.1. For example, these peptides

may include any of the additional amin -terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "Z" groups.

5 Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions
10 and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section
15 5.2.

15 Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory
20 Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX
25 presents Human Parainfluenza Virus 3 F1 region DP178 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and
30 Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped
35 according to the specific virus which they inhibit,

including respiratory syncytial virus, human
parainfluenza virus 3, simian immunodeficiency virus
and measles virus.

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TABLE V

ALLMOT15 SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

PCGENE	ALLNOTES	AB Virus (see Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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[illegible]

All Viruses (see bacteriophages)		AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PCGENE	ALLNOTES								
FILE NAME	PROTEIN								
PCOAT_1A1M1	COAT PROTEIN	64-100							
PCOAT_1A1M2	COAT PROTEIN	128-166							
PCOAT_1A1M3	COAT PROTEIN	5-40							
PCOAT_1A1M4	COAT PROTEIN	38-72							
PCOAT_1A1M5	COAT PROTEIN	7-35							
PCOAT_1A1M6	GENOME POLYPROTEIN	14-48							
PCOAT_1A1M7	COAT PROTEIN	1-37	43-77						
PCOAT_1A1M8	COAT PROTEIN	44-78	100-134						
PCOAT_1A1M9	COAT PROTEIN	13-46							
PCOAT_1A1M10	COAT PROTEIN	186-220							
PCOAT_1A1M11	COAT PROTEIN	101-137							
PCOAT_1A1M12	COAT PROTEIN	101-137							
PCOAT_1A1M13	COAT PROTEIN	103-137							
PCOAT_1A1M14	COAT PROTEIN	76-138							
PCOAT_1A1M15	COAT PROTEIN	101-137							
PCOAT_1A1M16	COAT PROTEIN	101-137							
PCOAT_1A1M17	COAT PROTEIN	101-137							
PCOAT_1A1M18	COAT PROTEIN	101-137							
PCOAT_1A1M19	COAT PROTEIN	101-137							
PCOAT_1A1M20	COAT PROTEIN	101-137							
PCOAT_1A1M21	COAT PROTEIN	71-109							
PCOAT_1A1M22	COAT PROTEIN	60-103							
PCOAT_1A1M23	COAT PROTEIN	2-36							
PCOAT_1A1M24	COAT PROTEIN	41-75							
PCOAT_1A1M25	COAT PROTEIN	41-75							
PCOAT_1A1M26	COAT PROTEIN	183-197							
PCOAT_1A1M27	COAT PROTEIN	94-135							
PCOAT_1A1M28	COAT PROTEIN	111-149							
PCOAT_1A1M29	COAT PROTEIN	62-106							
PCOAT_1A1M30	COAT PROTEIN	42-106							
PCOAT_1A1M31	COAT PROTEIN	198-232							
PCOAT_1A1M32	COAT PROTEIN	291-336							
PCOAT_1A1M33	COAT PROTEIN	291-336							
PCOAT_1A1M34	COAT PROTEIN	213-332							
PCOAT_1A1M35	COAT PROTEIN	318-372							
PCOAT_1A1M36	COAT PROTEIN	535-595							
PCOAT_1A1M37	COAT PROTEIN	535-595							
PCOAT_1A1M38	COAT PROTEIN	535-595							
PCOAT_1A1M39	COAT PROTEIN	535-595							
PCOAT_1A1M40	COAT PROTEIN	535-595							
PCOAT_1A1M41	COAT PROTEIN	535-595							
PCOAT_1A1M42	COAT PROTEIN	535-595							
PCOAT_1A1M43	COAT PROTEIN	535-595							
PCOAT_1A1M44	COAT PROTEIN	535-595							
PCOAT_1A1M45	COAT PROTEIN	535-595							
PCOAT_1A1M46	COAT PROTEIN	535-595							
PCOAT_1A1M47	COAT PROTEIN	535-595							
PCOAT_1A1M48	COAT PROTEIN	535-595							
PCOAT_1A1M49	COAT PROTEIN	535-595							
PCOAT_1A1M50	COAT PROTEIN	535-595							
PCOAT_1A1M51	COAT PROTEIN	535-595							
PCOAT_1A1M52	COAT PROTEIN	535-595							
PCOAT_1A1M53	COAT PROTEIN	535-595							
PCOAT_1A1M54	COAT PROTEIN	535-595							
PCOAT_1A1M55	COAT PROTEIN	535-595							
PCOAT_1A1M56	COAT PROTEIN	535-595							
PCOAT_1A1M57	COAT PROTEIN	535-595							
PCOAT_1A1M58	COAT PROTEIN	535-595							
PCOAT_1A1M59	COAT PROTEIN	535-595							
PCOAT_1A1M60	COAT PROTEIN	535-595							
PCOAT_1A1M61	COAT PROTEIN	535-595							
PCOAT_1A1M62	COAT PROTEIN	535-595							
PCOAT_1A1M63	COAT PROTEIN	535-595							
PCOAT_1A1M64	COAT PROTEIN	535-595							
PCOAT_1A1M65	COAT PROTEIN	535-595							
PCOAT_1A1M66	COAT PROTEIN	535-595							
PCOAT_1A1M67	COAT PROTEIN	535-595							
PCOAT_1A1M68	COAT PROTEIN	535-595							
PCOAT_1A1M69	COAT PROTEIN	535-595							
PCOAT_1A1M70	COAT PROTEIN	535-595							
PCOAT_1A1M71	COAT PROTEIN	535-595							
PCOAT_1A1M72	COAT PROTEIN	535-595							
PCOAT_1A1M73	COAT PROTEIN	535-595							
PCOAT_1A1M74	COAT PROTEIN	535-595							
PCOAT_1A1M75	COAT PROTEIN	535-595							
PCOAT_1A1M76	COAT PROTEIN	535-595							
PCOAT_1A1M77	COAT PROTEIN	535-595							
PCOAT_1A1M78	COAT PROTEIN	535-595							
PCOAT_1A1M79	COAT PROTEIN	535-595							
PCOAT_1A1M80	COAT PROTEIN	535-595							
PCOAT_1A1M81	COAT PROTEIN	535-595							
PCOAT_1A1M82	COAT PROTEIN	535-595							
PCOAT_1A1M83	COAT PROTEIN	535-595							
PCOAT_1A1M84	COAT PROTEIN	535-595							
PCOAT_1A1M85	COAT PROTEIN	535-595							
PCOAT_1A1M86	COAT PROTEIN	535-595							
PCOAT_1A1M87	COAT PROTEIN	535-595							
PCOAT_1A1M88	COAT PROTEIN	535-595							
PCOAT_1A1M89	COAT PROTEIN	535-595							
PCOAT_1A1M90	COAT PROTEIN	535-595							
PCOAT_1A1M91	COAT PROTEIN	535-595							
PCOAT_1A1M92	COAT PROTEIN	535-595							
PCOAT_1A1M93	COAT PROTEIN	535-595							
PCOAT_1A1M94	COAT PROTEIN	535-595							
PCOAT_1A1M95	COAT PROTEIN	535-595							
PCOAT_1A1M96	COAT PROTEIN	535-595							
PCOAT_1A1M97	COAT PROTEIN	535-595							
PCOAT_1A1M98	COAT PROTEIN	535-595							
PCOAT_1A1M99	COAT PROTEIN	535-595							
PCOAT_1A1M100	COAT PROTEIN	535-595							

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PCGENE		ALLMO713	All Viruses (see Bacteriophage)							
FILE NAME	PROTEIN		VIRUS	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FRIEND SPLEEN FOCUS-FORMING VIRUS	341-375						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FRIEND SPLEEN FOCUS-FORMING VIRUS	341-378						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	AVIAN NECROTIC DISEASE VIRUS	426-432						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	AVIAN NECROTIC DISEASE VIRUS	426-438						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	AVIAN NECROTIC DISEASE VIRUS (STRAIN MT)	190-416						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	BOVINE DAUNODENEFICIENCY VIRUS (ISOLATE 106)	10-44	81-122	221-335	330-410	631-691		
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	BOVINE DAUNODENEFICIENCY VIRUS (ISOLATE 117)	10-44	81-122	139-193	330-384	559-639	664-724	
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	BOVINE LEUKAEMIA VIRUS (AMERICAN ISOLATE FLK)	304-379						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	BOVINE LEUKAEMIA VIRUS (AUSTRALIAN ISOLATE)	304-379						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	BOVINE LEUKAEMIA VIRUS (AMERICAN ISOLATE VDM)	304-379						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	BOVINE LEUKAEMIA VIRUS (BELGIAN ISOLATE LB59)	304-379						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	BOVINE LEUKAEMIA VIRUS (JAPANESE ISOLATE N-5-1)	304-379						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	CAPRIAN ARTHRITIS ENCEPHALITIS VIRUS (STRAIN CORK)	137-196	615-726	715-781	843-905			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	CAPRIAN ARTHRITIS ENCEPHALITIS VIRUS (STRAIN GA)	134-193	611-710	716-783	843-905			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-1)	18-76	416-535	519-593	668-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-3)	18-76	416-535	519-593	658-693			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-5)	18-76	416-535	519-593	658-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE P3 2-5)	18-76	416-535	519-593	658-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (CLONE CL23)	18-76	416-535	519-593	658-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEMIA VIRUS (STRAIN WYOMING)	18-76	416-535	519-593	658-716			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FELINE ENDOGENOUS VIRUS ECE1	501-555	567-604					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FELINE DAUNODENEFICIENCY VIRUS (ISOLATE PETALUSIA)	610-690	715-716					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FELINE DAUNODENEFICIENCY VIRUS (ISOLATE SAN DIEGO)	601-681	715-716					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FELINE DAUNODENEFICIENCY VIRUS (ISOLATE TINI)	601-681	715-716					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FELINE LEUKAEMIA VIRUS (STRAIN LAUMDA-81)	475-537	516-573					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FELINE LEUKAEMIA VIRUS (STRAIN SARMIA)	1-41	134-203	211-335	361-493	864-901		
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FELINE LEUKAEMIA VIRUS (STRAIN GADSDNER-ADAMSTEN)	498-550	562-596					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FELINE LEUKAEMIA VIRUS (STRAIN GA)	478-536	562-576					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FELINE LEUKAEMIA VIRUS (STRAIN SM)	481-536	545-579					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	FELINE LEUKAEMIA VIRUS (STRAIN SMYDNER-THEILER)	498-532						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	GIBBON APE LEUKAEMIA VIRUS	521-575	587-621					
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN T-CELL LEUKAEMIA VIRUS TYPE I (STRAIN ATL)	211-383						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN T-CELL LEUKAEMIA VIRUS TYPE I (ISOLATE MT-2)	211-383						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN T-CELL LEUKAEMIA VIRUS TYPE II	317-377						
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (ANV552) ISOLATE	497-593	612-711	764-841				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (BHI10) ISOLATE	505-594	610-712	761-843				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (BHI10) ISOLATE	505-594	665-767	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (BRAIN ISOLATE)	311-365	501-590	609-708	761-831			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (BRAIN ISOLATE)	311-365	615-717	771-841				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (CD3-41) ISOLATE	312-376	510-606	626-726	779-855			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (ELI) ISOLATE	315-396	502-591	607-709	761-839			
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				
ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	ENV POLYPROTEIN PRECURSOR	HUMAN DAUNODENEFICIENCY VIRUS TYPE I (HXB3) ISOLATE	305-594	610-712	761-838				

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PCGENE	ALLNOTES	ALL Viroes (no better description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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PCGENE	ALL MOTIFS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
AB Viruses (see bacteriophages)									
PROTEIN	YINUS								
PRO2.3 BAYM1	BANLEY YELLOW MOSAIC VIRUS (JAPANESE STRAIN II-1)	649-733	716-773	787-828					
PRO2.3 GFLV	GRAPEVINE FANLEAF VIRUS	383-406	347-402						
PRO2.3 TRVS		6-38							
PRO2.3 TSVR	TOMATO BLACK RING VIRUS (STRAIN S)	338-206	334-168						
PRO2.3 ROVEV	TOMATO RINGSPOOT VIRUS (ISOLATE MASPERRY)	349-886	1382-1416	1458-1507	1376-1617				
PRO2.3 BYDVN	BOYDVE ENTEROVIRUS (STRAIN VG-2-37)	244-289	1008-1064	1033-1074	1803-1344	1392-1443	1869-1910	2326-2360	
PRO2.3 BYDVN	BOYDVE VIRAL DIARRHEA VIRUS (ISOLATE NADL)	245-289	639-663	639-663	1033-1074	1392-1443	1778-1820	2316-2370	
PRO2.3 BYDVN	BOYDVE VIRAL DIARRHEA VIRUS (STRAIN SD-1)	245-289	646-691	646-691	1033-1074	1392-1443	1778-1820	2316-2370	
PRO2.3 BYDVN	BEAN YELLOW MOSAIC VIRUS	96-130							
PRO2.3 BYDVN	COSACKIEVIRUS A31 (STRAIN COE)	9-43	363-396	664-698	1043-1100	1607-1648	1805-1839	1901-1946	
PRO2.3 COX43	COSACKIEVIRUS A9 (STRAIN GAUGGS)	13-49	1040-1084	1895-1940					
PRO2.3 COX49	COSACKIEVIRUS B1	13-49	1031-1087	1876-1921					
PRO2.3 COX83	COSACKIEVIRUS B1	13-49	1034-1070	1879-1924					
PRO2.3 COX84	COSACKIEVIRUS B4	13-49	643-681	1022-1068	1877-1922				
PRO2.3 COX84	COSACKIEVIRUS B5	13-49	1034-1070	1879-1924					
PRO2.3 CYVV	CLOVEE YELLOW VEIN VIRUS	126-134							
PRO2.3 DEN11	DENGUE VIRUS TYPE 1 (STRAIN 316-1)	74-108							
PRO2.3 DEN11	DENGUE VIRUS TYPE 1 (STRAIN A1F 81-40)	74-108							
PRO2.3 DEN11	DENGUE VIRUS TYPE 1 (STRAIN CY163697)	74-108	832-873	960-994	1143-1179	1614-1648	2318-2354	2946-3016	
PRO2.3 DEN1W	DENGUE VIRUS TYPE 1 (STRAIN WESTERN PACIFIC C)	74-108	833-874	961-995	1143-1180				
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (ISOLATE MALAYSIA M1)	448-493							
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (ISOLATE MALAYSIA M3)	448-493							
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (STRAIN 16481)	74-108	728-777	961-995	1146-1180	1264-1280	1615-1649	2317-2351	
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (STRAIN 16481-PDK33)	74-108	728-777	961-995	1146-1180	1264-1280	1615-1649	2317-2351	
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (STRAIN D3-94)	728-777							
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (STRAIN TH-24)	997-546							
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (STRAIN JAMAICA)	74-108	728-777	961-995	1146-1180	1264-1280	1615-1649	2317-2351	
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (STRAIN NEW GUINEA C)	217-247	358-432						
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (STRAIN FR13951)	74-108	728-777	961-995	1146-1180	1264-1280	1615-1649	2317-2351	
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (STRAIN TONGA 1974)	448-493	532-595	641-715	966-990	1265-1299	1615-1649	2317-2351	
PRO2.3 DEN1	DENGUE VIRUS TYPE 2 (STRAIN PUD-218)	614-663							
PRO2.3 DEN1	DENGUE VIRUS TYPE 3	810-872	959-993	1385-1419	2224-2218	2400-2321	2904-2978	3005-3014	
PRO2.3 DEN1	DENGUE VIRUS TYPE 4	957-993	1180-1414	2314-2355	2701-2733	2941-2975	3077-3011		
PRO2.3 DEN1	ECHOVIRUS 11 (STRAIN GREGORY)	217-247	1079-1113						
PRO2.3 ECTIG	ENCEPHALOMYOCARDITIS VIRUS	1074-1113	1472-1518	1522-1570	1665-1706	1789-1833			
PRO2.3 EMCV	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EMC-8 NONDIABETO)	145-179	1076-1117	1076-1120	1667-1708				
PRO2.3 EMCV	ENCEPHALOMYOCARDITIS VIRUS (STRAIN EMC-D DIABETOGEN)	145-179	1076-1117	1674-1526	1657-1708				
PRO2.3 EMCV	MENGO ENCEPHALOMYOCARDITIS VIRUS (STRAIN 11A)	145-179							
PRO2.3 ENH43	MENGO ENCEPHALOMYOCARDITIS VIRUS	78-112							
PRO2.3 ENH43	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A10-61)	221-255	294-328	378-412	1103-1153	1409-1528	2165-2300		
PRO2.3 FMDV1	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN A12)	220-254	291-327	377-411	1103-1164	1409-1528	2164-2199		
PRO2.3 FMDVA	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND OIBF3)	221-255	1103-1153	1409-1528	2164-2199				
PRO2.3 FMDVB	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN C1-SANTA PAU IC-5)	87-128	693-728						
PRO2.3 FMDVS	FOOT-AND-MOUTH DISEASE VIRUS (STRAIN C1)	221-255	281-317	377-411					
PRO2.3 FMDVT	HEPATITIS C VIRUS (ISOLATE 1)	364-398							
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN ALFORT)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-493	616-660	693-729	1071-1070	1190-1235	1307-1343	1799-1826	2136-2170
PRO2.3 HCVA	HOG CHOLERA VIRUS (STRAIN BRESICIA)	440-49							

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[illegible]

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GENE	ALLNOTIS	AB Viruses (see biotransporter)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
PROTEIN	PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	037-648					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AD4P)	94-110					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	HERPESVIRUS SAIMIRI (STRAIN 11)	324-365					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN COPENHAGEN)	367-402					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR)	367-402					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	367-402					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	327-237					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ERSTEIN-BABA VIRUS (STRAIN B91-4)	09-137					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	BOVINE HERPESVIRUS TYPE 1 (STRAIN 34)	101-135					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P)	106-140					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	HERPESVIRUS SAIMIRI (STRAIN 11)	125-159					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	SHOEPIBIONIA VIRUS (STRAIN KASZA)	08-132					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN COPENHAGEN)	08-132					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN L-1V9)	08-132					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR)	08-132					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	08-132					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG31)	171-212					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPENHAGEN)	116-150					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	41-75					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN COPENHAGEN)	243-291					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR)	243-291					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	243-291					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	CAPRIPOXVIRUS (STRAIN K.S. 1)	19-40					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	114-155					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	311-245					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPENHAGEN)	211-245					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	62-116					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	62-116					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN COPENHAGEN)	1-71					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	1-71					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPENHAGEN)	35-39					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	35-39					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VACCINIA VIRUS (STRAIN WR) AND (STRAIN COPENHAGEN)	40-93					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	VARICELLA VIRUS	43-93					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	LEISTAD VIRUS	1533-1587					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	EQUINE ARTERITIS VIRUS	1033-1117					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN ANANN ARBOR/640)	171-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN ABUEINGO/1154)	171-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN ADUNEDIN/477)	171-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AGULJAKAR/1 AND/70477)	171-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	INFLUENZA A VIRUS (STRAIN AEGUNDA/ONDON/114733)	168-242					
ADONUCLEOSIDE-DIPHOSPHATE REDUCTASE LAR	ADONUCLEOSIDE-DIPHOSPH							

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GENE	ALL MOTIFS	AB Viruses (see bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
TOBIACCO NECROSIS VIRUS (STRAIN D)	AREA1	102-144						
BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A1198)	AREA1	99-158	160-216					
CANINE DISTEMPER VIRUS (STRAIN ONDARSTEEPOORT)	AREA1	312-372						
HUMAN RESPIRATORY SYNCYTIAL VIRUS	AREA1	99-158	160-216					
HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP B / STRAIN 1)	AREA1	99-158	160-216					
HUMAN RESPIRATORY SYNCYTIAL VIRUS (STRAIN A2)	AREA1	99-158	160-216					
HUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAIN 1)	AREA1	99-158	160-216					
MEASLES VIRUS (STRAIN EDMONSTON)	AREA1	312-374	460-495					
MEASLES VIRUS (STRAIN IP-3-CA)	AREA1	312-374	460-495					
MEASLES VIRUS (STRAIN YAMAGATA-1)	AREA1	312-374	460-495					
MUMPS VIRUS (STRAIN SBL-1)	AREA1	140-183	212-275					
MUMPS VIRUS (STRAIN ENDELS)	AREA1	214-276						
MUMPS VIRUS (STRAIN MIYAHARA VACCINE)	AREA1	214-276						
NEWCASTLE DISEASE VIRUS (STRAIN AUSTRALIA-VICTORIA/73)	AREA1	100-134						
NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CH4)	AREA1	100-138						
HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	AREA1	80-114	375-437					
HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C19)	AREA1	80-114	375-437					
HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-377)	AREA1	80-114	375-437					
HUMAN PARAINFLUENZA 1 VIRUS (STRAIN C1-14/10)	AREA1	80-114	375-437					
HUMAN PARAINFLUENZA 2 VIRUS	AREA1	212-281						
HUMAN PARAINFLUENZA 2 VIRUS (STRAIN TOSHIBA)	AREA1	212-281						
BOVINE PARAINFLUENZA 3 VIRUS	AREA1	31-130	414-470					
HUMAN PARAINFLUENZA 3 VIRUS (STRAIN NIH 47815)	AREA1	410-499						
HUMAN PARAINFLUENZA 4A VIRUS (STRAIN TOSHIBA)	AREA1	4-38	222-285					
HUMAN PARAINFLUENZA 4B VIRUS (STRAIN 4B-322)	AREA1	222-285						
PINK VIRUS	AREA1	137-174						
RABIES VIRUS (STRAIN AVO1)	AREA1	93-127						
RABIES VIRUS (STRAIN CVS-11)	AREA1	93-127						
RABIES VIRUS (STRAIN ERA), AND (STRAIN PM)	AREA1	93-127						
RABIES VIRUS (STRAIN PV)	AREA1	93-127						
RABIES VIRUS (STRAIN SAD B19)	AREA1	93-127						
SENDAI VIRUS (STRAIN Z / HOST MUTANTS)	AREA1	312-364	375-447					
SENDAI VIRUS (STRAIN 604)	AREA1	312-364	375-447					
SENDAI VIRUS (STRAIN FUSH040)	AREA1	312-364	375-447					
SENDAI VIRUS (STRAIN HARRIS)	AREA1	312-364	375-447					
SENDAI VIRUS (STRAIN Z)	AREA1	312-364	375-447					
SENDAI VIRUS (STRAIN W1)	AREA1	205-278						
SONCHUS YELLOW NET VIRUS	AREA1	138-172	223-281					
VECTICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN C)	AREA1	1-43						
VECTICULAR STOMATITIS VIRUS (SEROTYPE INDIANA / STRAIN M)	AREA1	1-43						
VECTICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 1-37)	AREA1	1-43						
VECTICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRAIN 1-37)	AREA1	1-43						
VECTICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	AREA1	223-284						
VECTICULAR STOMATITIS VIRUS (STRAIN SAN JUAN)	AREA1	223-284						
AMSACTA MOOREI ENTOMOPHAGUS VIRUS	AREA1	21-36						
VACCINIA VIRUS (STRAIN WR)	AREA1	21-36						
VACCINIA VIRUS	AREA1	21-36						
VACCINIA VIRUS (STRAIN COFFERHAGEN)	AREA1	118-167	223-286					
VACCINIA VIRUS (STRAIN WR)	AREA1	118-167	223-286					

[illegible]

PGCENE	ALLNOTIS	AB Virus (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7
QLEPABIE	ALLNOTIS	VIRUS	492-491	492-491					
PTUN AV131	DNA TERMINAL PROTEIN	HUMAN ADENOVIRUS TYPE 12	210-284	210-284					
PTMAF AV134	TRANSFORMING PROTEIN RUN	AVIAN SARCOMA VIRUS (STRAIN 17)	217-288	217-288					
PTOP1 SVYKA	TRANSFORMING PROTEIN MAP	AVIAN MUSCULOPHOSPHOTIC FIBROSARCOMA VIRUS A343	269-310	269-310					
PTOP2 ASYB7	DNA TOPOISOMERASE	SHOPE FIBROMA VIRUS (STRAIN KASZA)	481-513	481-513					
PTOP2 ASYB7	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (STRAIN BA71V)	146-180	146-180					
PTIS5 SASAV	DNA TOPOISOMERASE II	AFRICAN SWINE FEVER VIRUS (ISOLATE MALAWI LIL 20V)	146-180	146-180					
PTYS3 VZVD	PDGF-RELATED TRANSFORMING PROTEIN P18-315	SODAN SARCOMA VIRUS	16-71	16-71					
PUBB1 NCYAP	THYADYLATE SYNTHASE	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	215-260	215-260					
PUB11 HCNVA	UBIQUITIN-LIKE PROTEIN	ORGYIA PSEUDOTRUGATA MULTICAPSID POLYDROSIS VIRUS	41-80	41-80					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	169-203	169-203					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	94-128	94-128					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HGS13)	92-126	92-126					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN AB47)	70-104	70-104					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	102-176	102-176					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN B91-4)	104-143	104-143					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	216-230	216-230					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	36-94	36-94					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	62-170	62-170					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPESVIRUS SAIMIRI (STRAIN 11)	90-140	90-140					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	27-111	27-111					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-50	6-50					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	174-208	174-208					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	122-163	122-163					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	47-81	47-81					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	202-243	202-243					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	32-96	32-96					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	PSEUDORABIES VIRUS (STRAIN NA-3)	41-95	41-95					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	61-103	61-103					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	266-300	266-300					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN AB47)	239-280	239-280					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN AB47)	44-78	44-78					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	213-233	213-233					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	5-39	5-39					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V8)	161-191	161-191					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	253-341	253-341					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	378-411	378-411					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	364-413	364-413					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPESVIRUS SAIMIRI (STRAIN 11)	29-92	29-92					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	INFECTIOUS LARYNGOTRACHEITIS VIRUS (STRAIN THORNE V8)	161-191	161-191					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	266-300	266-300					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	244-285	244-285					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	153-187	153-187					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	163-197	163-197					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	102-176	102-176					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	72-108	72-108					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (STRAIN DUMAS)	94-133	94-133					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	VARICELLA-ZOSTER VIRUS (STRAIN DUMAS)	29-43	29-43					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	EPSTEIN-BARR VIRUS (STRAIN B95-4)	139-200	139-200					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	113-147	113-147					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17)	187-221	187-221					
PUB10 HCNVA	HYPOTHETICAL PROTEIN UL1	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	231-268	231-268					

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PCGENE	ALLNOTES	AE Virus (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
FILE NAME	PROTEIN	VIRUS	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PUS01 HCV11	HYPOTHETICAL PROTEIN HCV11	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	84-125							
PUS02 HCV12	URACIL-DNA GLYCOSYLASE	HERPES SIMPLEX VIRUS (TYPE 1 (STRAIN 17))	227-264							
PUS03 HCV13	URACIL-DNA GLYCOSYLASE	HERPES SIMPLEX VIRUS (TYPE 2 (STRAIN 31))	188-219							
PUS04 HCV14	URACIL-DNA GLYCOSYLASE	HERPES SIMPLEX VIRUS (TYPE 3 (STRAIN 1053))	148-189							
PUS05 HCV15	URACIL-DNA GLYCOSYLASE	HERPESVIRUS SANGUI (STRAIN 11)	135-176							
PUS06 HCV16	URACIL-DNA GLYCOSYLASE	SHOPE FIBROBLAST VIRUS (STRAIN KASZA)	81-113							
PUS07 HCV17	URACIL-DNA GLYCOSYLASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN AB47)	79-120							
PUS08 HCV18	URACIL-DNA GLYCOSYLASE	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTUCKY A)	84-120							
PUS09 HCV19	URACIL-DNA GLYCOSYLASE		2-16							
PUS10 HCV20	HYPOTHETICAL PROTEIN HCV20	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)								
PUS11 HCV21	HYPOTHETICAL PROTEIN HCV21	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	3-51							
PUS12 HCV22	HYPOTHETICAL PROTEIN HCV22	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	187-225							
PUS13 HCV23	MEMBRANE PROTEIN HCV23	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	284-315		335-378					
PUS14 HCV24	HYPOTHETICAL PROTEIN HCV24	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-172							
PUS15 HCV25	HYPOTHETICAL PROTEIN HCV25	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	335-384							
PUS16 HCV26	HYPOTHETICAL PROTEIN HCV26	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	6-40							
PUS17 HCV27	G-PROTEIN COUPLED RECEPTOR HOMOLOG US37	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	135-169		274-312					
PUS18 HCV28	HYPOTHETICAL PROTEIN HCV28	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	18-52		326-367		391-449			
PUS19 HCV29	HELICASE	ALFALFA MOSAIC VIRUS (STRAIN 4257 ISOLATE LEIDEN)	313-350		1114-1150		1179-1213			
PUS20 HCV30	18 KD PROTEIN	TOBACCO BATTLE VIRUS (STRAIN P50)	35-117							
PUS21 HCV31	16 KD PROTEIN	TOBACCO BATTLE VIRUS (STRAIN SYN)	35-117							
PUS22 HCV32	1A PROTEIN	BROAD BEAN MOTTLE VIRUS	21-55		349-403		492-526			
PUS23 HCV33	1A PROTEIN	BROME MOSAIC VIRUS	4-46		348-411				990-924	
PUS24 HCV34	1A PROTEIN	COMPEX CHLOROTIC MOTTLE VIRUS	4-53		212-276		348-389			
PUS25 HCV35	1A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	11-44		393-434		584-619		497-526	
PUS26 HCV36	1A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN O)	11-44		393-434		584-619		848-916	
PUS27 HCV37	1A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Q)	11-44		393-434		584-619		848-916	
PUS28 HCV38	1A PROTEIN	PEANUT STUNT VIRUS (STRAIN J)	4-46		393-434					
PUS29 HCV39	1A PROTEIN	TOMATO ASPERMATY VIRUS	11-59		392-433		557-592			
PUS30 HCV40	1A PROTEIN	TURKEY HERPESVIRUS (STRAIN 12)	177-211							
PUS31 HCV41	32.3 KD PROTEIN	BODNA DISEASE VIRUS	63-121		100-171					
PUS32 HCV42	24 KD ANTIGEN	AUTOGRAHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	4-50							
PUS33 HCV43	33 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN 1)	116-150							
PUS34 HCV44	38 KD PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	116-150							
PUS35 HCV45	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS36 HCV46	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS37 HCV47	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS38 HCV48	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS39 HCV49	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS40 HCV50	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS41 HCV51	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS42 HCV52	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS43 HCV53	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS44 HCV54	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS45 HCV55	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS46 HCV56	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS47 HCV57	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS48 HCV58	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS49 HCV59	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS50 HCV60	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS51 HCV61	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS52 HCV62	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS53 HCV63	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS54 HCV64	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS55 HCV65	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS56 HCV66	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS57 HCV67	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS58 HCV68	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS59 HCV69	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS60 HCV70	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS61 HCV71	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS62 HCV72	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS63 HCV73	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS64 HCV74	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS65 HCV75	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS66 HCV76	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS67 HCV77	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS68 HCV78	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS69 HCV79	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS70 HCV80	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS71 HCV81	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS72 HCV82	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS73 HCV83	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS74 HCV84	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS75 HCV85	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS76 HCV86	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS77 HCV87	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS78 HCV88	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS79 HCV89	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS80 HCV90	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS81 HCV91	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS82 HCV92	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS83 HCV93	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS84 HCV94	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS85 HCV95	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS86 HCV96	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS87 HCV97	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS88 HCV98	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS89 HCV99	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							
PUS90 HCV100	38 KD PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN LIS37)	138-183							

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PLASMID	ALLIOTIS	ALL VIRUSES (no bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
PROTEIN	PROTEIN	VIRUS								
PROTEIN A1	PROTEIN A1	VIRUS	62-96	143-184						
PROTEIN A2	PROTEIN A2	VIRUS	3-40	126-160						
PROTEIN A3	PROTEIN A3	VIRUS	3-40	126-160						
PROTEIN A4	PROTEIN A4	VIRUS	3-40	126-160						
PROTEIN A5	PROTEIN A5	VIRUS	91-132							
PROTEIN A6	PROTEIN A6	VIRUS	91-132							
PROTEIN A7	PROTEIN A7	VIRUS	134-168							
PROTEIN A8	PROTEIN A8	VIRUS	210-269							
PROTEIN A9	PROTEIN A9	VIRUS	221-262							
PROTEIN A10	PROTEIN A10	VIRUS	221-262							
PROTEIN A11	PROTEIN A11	VIRUS	117-131							
PROTEIN A12	PROTEIN A12	VIRUS	191-235							
PROTEIN A13	PROTEIN A13	VIRUS	44-78	93-124						
PROTEIN A14	PROTEIN A14	VIRUS	44-78	93-124						
PROTEIN A15	PROTEIN A15	VIRUS	10-78	87-121						
PROTEIN A16	PROTEIN A16	VIRUS	46-80	91-125						
PROTEIN A17	PROTEIN A17	VIRUS	44-78							
PROTEIN A18	PROTEIN A18	VIRUS	22-70	84-127						
PROTEIN A19	PROTEIN A19	VIRUS	22-70	93-127						
PROTEIN A20	PROTEIN A20	VIRUS	22-70	93-127						
PROTEIN A21	PROTEIN A21	VIRUS	22-70	93-127						
PROTEIN A22	PROTEIN A22	VIRUS	22-70	93-127						
PROTEIN A23	PROTEIN A23	VIRUS	22-70	93-127						
PROTEIN A24	PROTEIN A24	VIRUS	22-70	93-127						
PROTEIN A25	PROTEIN A25	VIRUS	22-70	93-127						
PROTEIN A26	PROTEIN A26	VIRUS	22-70	93-127						
PROTEIN A27	PROTEIN A27	VIRUS	22-70	93-127						
PROTEIN A28	PROTEIN A28	VIRUS	22-70	93-127						
PROTEIN A29	PROTEIN A29	VIRUS	22-70	93-127						
PROTEIN A30	PROTEIN A30	VIRUS	22-70	93-127						
PROTEIN A31	PROTEIN A31	VIRUS	22-70	93-127						
PROTEIN A32	PROTEIN A32	VIRUS	22-70	93-127						
PROTEIN A33	PROTEIN A33	VIRUS	22-70	93-127						
PROTEIN A34	PROTEIN A34	VIRUS	22-70	93-127						
PROTEIN A35	PROTEIN A35	VIRUS	22-70	93-127						
PROTEIN A36	PROTEIN A36	VIRUS	22-70	93-127						
PROTEIN A37	PROTEIN A37	VIRUS	22-70	93-127						
PROTEIN A38	PROTEIN A38	VIRUS	22-70	93-127						
PROTEIN A39	PROTEIN A39	VIRUS	22-70	93-127						
PROTEIN A40	PROTEIN A40	VIRUS	22-70	93-127						
PROTEIN A41	PROTEIN A41	VIRUS	22-70	93-127						
PROTEIN A42	PROTEIN A42	VIRUS	22-70	93-127						
PROTEIN A43	PROTEIN A43	VIRUS	22-70	93-127						
PROTEIN A44	PROTEIN A44	VIRUS	22-70	93-127						
PROTEIN A45	PROTEIN A45	VIRUS	22-70	93-127						
PROTEIN A46	PROTEIN A46	VIRUS	22-70	93-127						
PROTEIN A47	PROTEIN A47	VIRUS	22-70	93-127						
PROTEIN A48	PROTEIN A48	VIRUS	22-70	93-127						
PROTEIN A49	PROTEIN A49	VIRUS	22-70	93-127						
PROTEIN A50	PROTEIN A50	VIRUS	22-70	93-127						
PROTEIN A51	PROTEIN A51	VIRUS	22-70	93-127						
PROTEIN A52	PROTEIN A52	VIRUS	22-70	93-127						
PROTEIN A53	PROTEIN A53	VIRUS	22-70	93-127						
PROTEIN A54	PROTEIN A54	VIRUS	22-70	93-127						
PROTEIN A55	PROTEIN A55	VIRUS	22-70	93-127						
PROTEIN A56	PROTEIN A56	VIRUS	22-70	93-127						
PROTEIN A57	PROTEIN A57	VIRUS	22-70	93-127						
PROTEIN A58	PROTEIN A58	VIRUS	22-70	93-127						
PROTEIN A59	PROTEIN A59	VIRUS	22-70	93-127						
PROTEIN A60	PROTEIN A60	VIRUS	22-70	93-127						
PROTEIN A61	PROTEIN A61	VIRUS	22-70	93-127						
PROTEIN A62	PROTEIN A62	VIRUS	22-70	93-127						
PROTEIN A63	PROTEIN A63	VIRUS	22-70	93-127						
PROTEIN A64	PROTEIN A64	VIRUS	22-70	93-127						
PROTEIN A65	PROTEIN A65	VIRUS	22-70	93-127						
PROTEIN A66	PROTEIN A66	VIRUS	22-70	93-127						
PROTEIN A67	PROTEIN A67	VIRUS	22-70	93-127						
PROTEIN A68	PROTEIN A68	VIRUS	22-70	93-127						
PROTEIN A69	PROTEIN A69	VIRUS	22-70	93-127						
PROTEIN A70	PROTEIN A70	VIRUS	22-70	93-127						
PROTEIN A71	PROTEIN A71	VIRUS	22-70	93-127						
PROTEIN A72	PROTEIN A72	VIRUS	22-70	93-127						
PROTEIN A73	PROTEIN A73	VIRUS	22-70	93-127						
PROTEIN A74	PROTEIN A74	VIRUS	22-70	93-127						
PROTEIN A75	PROTEIN A75	VIRUS	22-70	93-127						
PROTEIN A76	PROTEIN A76	VIRUS	22-70	93-127						
PROTEIN A77	PROTEIN A77	VIRUS	22-70	93-127						
PROTEIN A78	PROTEIN A78	VIRUS	22-70	93-127						
PROTEIN A79	PROTEIN A79	VIRUS	22-70	93-127						
PROTEIN A80	PROTEIN A80	VIRUS	22-70	93-127						
PROTEIN A81	PROTEIN A81	VIRUS	22-70	93-127						
PROTEIN A82	PROTEIN A82	VIRUS	22-70	93-127						
PROTEIN A83	PROTEIN A83	VIRUS	22-70	93-127						
PROTEIN A84	PROTEIN A84	VIRUS	22-70	93-127						
PROTEIN A85	PROTEIN A85	VIRUS	22-70	93-127						
PROTEIN A86	PROTEIN A86	VIRUS	22-70	93-127						
PROTEIN A87	PROTEIN A87	VIRUS	22-70	93-127						
PROTEIN A88	PROTEIN A88	VIRUS	22-70	93-127						
PROTEIN A89	PROTEIN A89	VIRUS	22-70	93-127						
PROTEIN A90	PROTEIN A90	VIRUS	22-70	93-127						
PROTEIN A91	PROTEIN A91	VIRUS	22-70	93-127						
PROTEIN A92	PROTEIN A92	VIRUS	22-70	93-127						
PROTEIN A93	PROTEIN A93	VIRUS	22-70	93-127						
PROTEIN A94	PROTEIN A94	VIRUS	22-70	93-127						
PROTEIN A95	PROTEIN A95	VIRUS	22-70	93-127						
PROTEIN A96	PROTEIN A96	VIRUS	22-70	93-127						
PROTEIN A97	PROTEIN A97	VIRUS	22-70	93-127						
PROTEIN A98	PROTEIN A98	VIRUS	22-70	93-127						
PROTEIN A99	PROTEIN A99	VIRUS	22-70	93-127						
PROTEIN A100	PROTEIN A100	VIRUS	22-70	93-127						
PROTEIN B1	PROTEIN B1	VIRUS	22-70	93-127						
PROTEIN B2	PROTEIN B2	VIRUS	22-70	93-127						
PROTEIN B3	PROTEIN B3	VIRUS	22-70	93-127						
PROTEIN B4	PROTEIN B4	VIRUS	22-70	93-127						
PROTEIN B5	PROTEIN B5	VIRUS	22-70	93-127						
PROTEIN B6	PROTEIN B6	VIRUS	22-70	93-127						
PROTEIN B7	PROTEIN B7	VIRUS	22-70	93-127						
PROTEIN B8	PROTEIN B8	VIRUS	22-70	93-127						
PROTEIN B9	PROTEIN B9	VIRUS	22-70	93-127						
PROTEIN B10	PROTEIN B10	VIRUS	22-70	93-127						
PROTEIN B11	PROTEIN B11	VIRUS	22-70	93-127						
PROTEIN B12	PROTEIN B12	VIRUS	22-70	93-127						
PROTEIN B13	PROTEIN B13	VIRUS	22-70	93-127						
PROTEIN B14	PROTEIN B14	VIRUS	22-70	93-127						
PROTEIN B15	PROTEIN B15	VIRUS	22-70	93-127						
PROTEIN B16	PROTEIN B16	VIRUS	22-70	93-127						
PROTEIN B17	PROTEIN B17	VIRUS	22-70	93-127						
PROTEIN B18	PROTEIN B18	VIRUS	22-70	93-127						
PROTEIN B19	PROTEIN B19	VIRUS	22-70	93-127						
PROTEIN B20	PROTEIN B20	VIRUS	22-70	93-127						
PROTEIN B21	PROTEIN B21	VIRUS	22-70	93-127						
PROTEIN B22	PROTEIN B22	VIRUS	22-70	93-127						
PROTEIN B23	PROTEIN B23	VIRUS	22-70	93-127						
PROTEIN B24	PROTEIN B24	VIRUS	22-70	93-127						
PROTEIN B25	PROTEIN B25	VIRUS	22-70	93-127						
PROTEIN B26	PROTEIN B26	VIRUS	22-70	93-127						
PROTEIN B27	PROTEIN B27	VIRUS	22-70	93-127						
PROTEIN B28	PROTEIN B28	VIRUS	22-70	93-127						
PROTEIN B29	PROTEIN B29	VIRUS	22-70	93-127						
PROTEIN B30	PROTEIN B30	VIRUS	22-70	93-127						
PROTEIN B31	PROTEIN B31	VIRUS	22-70	93-127						
PROTEIN B32	PROTEIN B32	VIRUS	22-70	93-127						
PROTEIN B33	PROTEIN B33	VIRUS	22-70	93-127						
PROTEIN B34	PROTEIN B34	VIRUS	22-70	93-127						
PROTEIN B35	PROTEIN B35	VIRUS	22-70	93-127						
PROTEIN B36	PROTEIN B36	VIRUS	22-70	93-127						
PROTEIN B37	PROTEIN B37	VIRUS	22-70	93-127						
PROTEIN B38	PROTEIN B38	VIRUS	22-70	93-127						
PROTEIN B39	PROTEIN B39	VIRUS	22-70	93-127						
PROTEIN B40	PROTEIN B40	VIRUS	22-70	93-127						
PROTEIN B41	PROTEIN B41	VIRUS	22-70	93-127						
PROTEIN B42	PROTEIN B42	VIRUS	22-70	93-127						
PROTEIN B43	PROTEIN B43	VIRUS	22-70	93-127						
PROTEIN B44	PROTEIN B44	VIRUS	22-70	93-127						
PROTEIN B45	PROTEIN B45	VIRUS	22-70	93-127						
PROTEIN B46	PROTEIN B46	VIRUS	22-70	93-127						
PROTEIN B47	PROTEIN B47	VIRUS	22-70	93-127						
PROTEIN B48	PROTEIN B48	VIRUS	22-70	93-127						
PROTEIN B49	PROTEIN B49	VIRUS	22-70	93-127						
PROTEIN B50	PROTEIN B50	VIRUS	22-70	93-127						
PROTEIN B51	PROTEIN B51	VIRUS	22-70	93-127						
PROTEIN B52	PROTEIN B52	VIRUS	22-70	93-127						
PROTEIN B53	PROTEIN B53	VIRUS	22-70	93-127						
PROTEIN B54	PROTEIN B54	VIRUS	22-70	93-127						
PROTEIN B55	PROTEIN B55	VIRUS	22-70	93-127						
PROTEIN B56	PROTEIN B56	VIRUS	22-70	93-127						
PROTEIN B57	PROTEIN B57	VIRUS	22-70	93-127						
PROTEIN B58	PROTEIN B58	VIRUS	22-70	93-127						

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[illegible]

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GENE		PROTEIN	AB Virus (see Description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500
GENE	PROTEIN	AB Virus (see Description)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	

90

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GENE	ALL VITIS	ALL VITIS (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PRP1	PRP1	PRP1	1-42							
PRP2	PRP2	PRP2	1-42							
PRP3	PRP3	PRP3	1-42							
PRP4	PRP4	PRP4	1-42							
PRP5	PRP5	PRP5	1-42							
PRP6	PRP6	PRP6	1-42							
PRP7	PRP7	PRP7	1-42							
PRP8	PRP8	PRP8	1-42							
PRP9	PRP9	PRP9	1-42							
PRP10	PRP10	PRP10	1-42							
PRP11	PRP11	PRP11	1-42							
PRP12	PRP12	PRP12	1-42							
PRP13	PRP13	PRP13	1-42							
PRP14	PRP14	PRP14	1-42							
PRP15	PRP15	PRP15	1-42							
PRP16	PRP16	PRP16	1-42							
PRP17	PRP17	PRP17	1-42							
PRP18	PRP18	PRP18	1-42							
PRP19	PRP19	PRP19	1-42							
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PRP21	PRP21	PRP21	1-42							
PRP22	PRP22	PRP22	1-42							
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PRP99	PRP99	PRP99	1-42							
PRP100	PRP100	PRP100	1-42							
PRP101	PRP101	PRP101	1-42							
PRP102	PRP102	PRP102	1-42							
PRP103	PRP103	PRP103	1-42							
PRP104	PRP104	PRP104	1-42							
PRP105	PRP105	PRP105	1-42							
PRP106	PRP106	PRP106	1-42							
PRP107	PRP107	PRP107	1-42							
PRP108	PRP108	PRP108	1-42							
PRP109	PRP109	PRP109	1-42							
PRP110	PRP110	PRP110	1-42							
PRP111	PRP111	PRP111	1-42							
PRP112	PRP112	PRP112	1-42							
PRP113	PRP113	PRP113	1-42							
PRP114	PRP114	PRP114	1-42							
PRP115	PRP115	PRP115	1-42							
PRP116	PRP116	PRP116	1-42							
PRP117	PRP117	PRP117	1-42							
PRP118	PRP118	PRP118	1-42							
PRP119	PRP119	PRP119	1-42							
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PRP126	PRP126	PRP126	1-42							
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PRP131	PRP131	PRP131	1-42							
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PRP136	PRP136	PRP136	1-42							
PRP137	PRP137	PRP137	1-42							
PRP138	PRP138	PRP138	1-42							
PRP139	PRP139	PRP139	1-42							
PRP140	PRP140	PRP140	1-42							
PRP141	PRP141	PRP141	1-42							
PRP142	PRP142	PRP142	1-42							
PRP143	PRP143	PRP143	1-42							
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PRP145	PRP145	PRP145	1-42							
PRP146	PRP146	PRP146	1-42							
PRP147	PRP147	PRP147	1-42							
PRP148	PRP148	PRP148	1-42							
PRP149	PRP149	PRP149	1-42							
PRP150	PRP150	PRP150	1-42							
PRP151	PRP151	PRP151	1-42							
PRP152	PRP152	PRP152	1-42							
PRP153	PRP153	PRP153	1-42							
PRP154	PRP154	PRP154	1-42							
PRP155	PRP155	PRP155	1-42							
PRP156	PRP156	PRP156	1-42							
PRP157	PRP157	PRP157	1-42							
PRP158	PRP158	PRP158	1-42							
PRP159	PRP159	PRP159	1-42							
PRP160	PRP160	PRP160	1-42							
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PRP163	PRP163	PRP163	1-42							
PRP164	PRP164	PRP164	1-42							
PRP165	PRP165	PRP165	1-42							
PRP166	PRP166	PRP166	1-42							
PRP167	PRP167	PRP167	1-42							
PRP168	PRP168	PRP168	1-42							
PRP169	PRP169	PRP169	1-42							
PRP170	PRP170	PRP170	1-42							
PRP171	PRP171	PRP171	1-42							
PRP172										

GENE	ALLIOTIS	AB Virus (no bacteriophage)	ABCA1	ABCA2	ABCA3	ABCA4	ABCA5	ABCA6	ABCA7	ABCA8	ABCA9	ABCA10	ABCA11	ABCA12	ABCA13	ABCA14	ABCA15	ABCA16	ABCA17	ABCA18	ABCA19	ABCA20	ABCA21	ABCA22	ABCA23	ABCA24	ABCA25	ABCA26	ABCA27	ABCA28	ABCA29	ABCA30	ABCA31	ABCA32	ABCA33	ABCA34	ABCA35	ABCA36	ABCA37	ABCA38	ABCA39	ABCA40	ABCA41	ABCA42	ABCA43	ABCA44	ABCA45	ABCA46	ABCA47	ABCA48	ABCA49	ABCA50	ABCA51	ABCA52	ABCA53	ABCA54	ABCA55	ABCA56	ABCA57	ABCA58	ABCA59	ABCA60	ABCA61	ABCA62	ABCA63	ABCA64	ABCA65	ABCA66	ABCA67	ABCA68	ABCA69	ABCA70	ABCA71	ABCA72	ABCA73	ABCA74	ABCA75	ABCA76	ABCA77	ABCA78	ABCA79	ABCA80	ABCA81	ABCA82	ABCA83	ABCA84	ABCA85	ABCA86	ABCA87	ABCA88	ABCA89	ABCA90	ABCA91	ABCA92	ABCA93	ABCA94	ABCA95	ABCA96	ABCA97	ABCA98	ABCA99	ABCA100	ABCA101	ABCA102	ABCA103	ABCA104	ABCA105	ABCA106	ABCA107	ABCA108	ABCA109	ABCA110	ABCA111	ABCA112	ABCA113	ABCA114	ABCA115	ABCA116	ABCA117	ABCA118	ABCA119	ABCA120	ABCA121	ABCA122	ABCA123	ABCA124	ABCA125	ABCA126	ABCA127	ABCA128	ABCA129	ABCA130	ABCA131	ABCA132	ABCA133	ABCA134	ABCA135	ABCA136	ABCA137	ABCA138	ABCA139	ABCA140	ABCA141	ABCA142	ABCA143	ABCA144	ABCA145	ABCA146	ABCA147	ABCA148	ABCA149	ABCA150	ABCA151	ABCA152	ABCA153	ABCA154	ABCA155	ABCA156	ABCA157	ABCA158	ABCA159	ABCA160	ABCA161	ABCA162	ABCA163	ABCA164	ABCA165	ABCA166	ABCA167	ABCA168	ABCA169	ABCA170	ABCA171	ABCA172	ABCA173	ABCA174	ABCA175	ABCA176	ABCA177	ABCA178	ABCA179	ABCA180	ABCA181	ABCA182	ABCA183	ABCA184	ABCA185	ABCA186	ABCA187	ABCA188	ABCA189	ABCA190	ABCA191	ABCA192	ABCA193	ABCA194	ABCA195	ABCA196	ABCA197	ABCA198	ABCA199	ABCA200	ABCA201	ABCA202	ABCA203	ABCA204	ABCA205	ABCA206	ABCA207	ABCA208	ABCA209	ABCA210	ABCA211	ABCA212	ABCA213	ABCA214	ABCA215	ABCA216	ABCA217	ABCA218	ABCA219	ABCA220	ABCA221	ABCA222	ABCA223	ABCA224	ABCA225	ABCA226	ABCA227	ABCA228	ABCA229	ABCA230	ABCA231	ABCA232	ABCA233	ABCA234	ABCA235	ABCA236	ABCA237	ABCA238	ABCA239	ABCA240	ABCA241	ABCA242	ABCA243	ABCA244	ABCA245	ABCA246	ABCA247	ABCA248	ABCA249	ABCA250	ABCA251	ABCA252	ABCA253	ABCA254	ABCA255	ABCA256	ABCA257	ABCA258	ABCA259	ABCA260	ABCA261	ABCA262	ABCA263	ABCA264	ABCA265	ABCA266	ABCA267	ABCA268	ABCA269	ABCA270	ABCA271	ABCA272	ABCA273	ABCA274	ABCA275	ABCA276	ABCA277	ABCA278	ABCA279	ABCA280	ABCA281	ABCA282	ABCA283	ABCA284	ABCA285	ABCA286	ABCA287	ABCA288	ABCA289	ABCA290	ABCA291	ABCA292	ABCA293	ABCA294	ABCA295	ABCA296	ABCA297	ABCA298	ABCA299	ABCA300	ABCA301	ABCA302	ABCA303	ABCA304	ABCA305	ABCA306	ABCA307	ABCA308	ABCA309	ABCA310	ABCA311	ABCA312	ABCA313	ABCA314	ABCA315	ABCA316	ABCA317	ABCA318	ABCA319	ABCA320	ABCA321	ABCA322	ABCA323	ABCA324	ABCA325	ABCA326	ABCA327	ABCA328	ABCA329	ABCA330	ABCA331	ABCA332	ABCA333	ABCA334	ABCA335	ABCA336	ABCA337	ABCA338	ABCA339	ABCA340	ABCA341	ABCA342	ABCA343	ABCA344	ABCA345	ABCA346	ABCA347	ABCA348	ABCA349	ABCA350	ABCA351	ABCA352	ABCA353	ABCA354	ABCA355	ABCA356	ABCA357	ABCA358	ABCA359	ABCA360	ABCA361	ABCA362	ABCA363	ABCA364	ABCA365	ABCA366	ABCA367	ABCA368	ABCA369	ABCA370	ABCA371	ABCA372	ABCA373	ABCA374	ABCA375	ABCA376	ABCA377	ABCA378	ABCA379	ABCA380	ABCA381	ABCA382	ABCA383	ABCA384	ABCA385	ABCA386	ABCA387	ABCA388	ABCA389	ABCA390	ABCA391	ABCA392	ABCA393	ABCA394	ABCA395	ABCA396	ABCA397	ABCA398	ABCA399	ABCA400	ABCA401	ABCA402	ABCA403	ABCA404	ABCA405	ABCA406	ABCA407	ABCA408	ABCA409	ABCA410	ABCA411	ABCA412	ABCA413	ABCA414	ABCA415	ABCA416	ABCA417	ABCA418	ABCA419	ABCA420	ABCA421	ABCA422	ABCA423	ABCA424	ABCA425	ABCA426	ABCA427	ABCA428	ABCA429	ABCA430	ABCA431	ABCA432	ABCA433	ABCA434	ABCA435	ABCA436	ABCA437	ABCA438	ABCA439	ABCA440	ABCA441	ABCA442	ABCA443	ABCA444	ABCA445	ABCA446	ABCA447	ABCA448	ABCA449	ABCA450	ABCA451	ABCA452	ABCA453	ABCA454	ABCA455	ABCA456	ABCA457	ABCA458	ABCA459	ABCA460	ABCA461	ABCA462	ABCA463	ABCA464	ABCA465	ABCA466	ABCA467	ABCA468	ABCA469	ABCA470	ABCA471	ABCA472	ABCA473	ABCA474	ABCA475	ABCA476	ABCA477	ABCA478	ABCA479	ABCA480	ABCA481	ABCA482	ABCA483	ABCA484	ABCA485	ABCA486	ABCA487	ABCA488	ABCA489	ABCA490	ABCA491	ABCA492	ABCA493	ABCA494	ABCA495	ABCA496	ABCA497	ABCA498	ABCA499	ABCA500	ABCA501	ABCA502	ABCA503	ABCA504	ABCA505	ABCA506	ABCA507	ABCA508	ABCA509	ABCA510	ABCA511	ABCA512	ABCA513	ABCA514	ABCA515	ABCA516	ABCA517	ABCA518	ABCA519	ABCA520	ABCA521	ABCA522	ABCA523	ABCA524	ABCA525	ABCA526	ABCA527	ABCA528	ABCA529	ABCA530	ABCA531	ABCA532	ABCA533	ABCA534	ABCA535	ABCA536	ABCA537	ABCA538	ABCA539	ABCA540	ABCA541	ABCA542	ABCA543	ABCA544	ABCA545	ABCA546	ABCA547	ABCA548	ABCA549	ABCA550	ABCA551	ABCA552	ABCA553	ABCA554	ABCA555	ABCA556	ABCA557	ABCA558	ABCA559	ABCA560	ABCA561	ABCA562	ABCA563	ABCA564	ABCA565	ABCA566	ABCA567	ABCA568	ABCA569	ABCA570	ABCA571	ABCA572	ABCA573	ABCA574	ABCA575	ABCA576	ABCA577	ABCA578	ABCA579	ABCA580	ABCA581	ABCA582	ABCA583	ABCA584	ABCA585	ABCA586	ABCA587	ABCA588	ABCA589	ABCA590	ABCA591	ABCA592	ABCA593	ABCA594	ABCA595	ABCA596	ABCA597	ABCA598	ABCA599	ABCA600	ABCA601	ABCA602	ABCA603	ABCA604	ABCA605	ABCA606	ABCA607	ABCA608	ABCA609	ABCA610	ABCA611	ABCA612	ABCA613	ABCA614	ABCA615	ABCA616	ABCA617	ABCA618	ABCA619	ABCA620	ABCA621	ABCA622	ABCA623	ABCA624	ABCA625	ABCA626	ABCA627	ABCA628	ABCA629	ABCA630	ABCA631	ABCA632	ABCA633	ABCA634	ABCA635	ABCA636	ABCA637	ABCA638	ABCA639	ABCA640	ABCA641	ABCA642	ABCA643	ABCA644	ABCA645	ABCA646	ABCA647	ABCA648	ABCA649	ABCA650	ABCA651	ABCA652	ABCA653	ABCA654	ABCA655	ABCA656	ABCA657	ABCA658	ABCA659	ABCA660	ABCA661	ABCA662	ABCA663	ABCA664	ABCA665	ABCA666	ABCA667	ABCA668	ABCA669	ABCA670	ABCA671	ABCA672	ABCA673	ABCA674	ABCA675	ABCA676	ABCA677	ABCA678	ABCA679	ABCA680	ABCA681	ABCA682	ABCA683	ABCA684	ABCA685	ABCA686	ABCA687	ABCA688	ABCA689	ABCA690	ABCA691	ABCA692	ABCA693	ABCA694	ABCA695	ABCA696	ABCA697	ABCA698	ABCA699	ABCA700	ABCA701	ABCA702	ABCA703	ABCA704	ABCA705	ABCA706	ABCA707	ABCA708	ABCA709	ABCA710	ABCA711	ABCA712	ABCA713	ABCA714	ABCA715	ABCA716	ABCA717	ABCA718	ABCA719	ABCA720	ABCA721	ABCA722	ABCA723	ABCA724	ABCA725	ABCA726	ABCA727	ABCA728	ABCA729	ABCA730	ABCA731	ABCA732	ABCA733	ABCA734	ABCA735	ABCA736	ABCA737	ABCA738	ABCA739	ABCA740	ABCA741	ABCA742	ABCA743	ABCA744	ABCA745	ABCA746	ABCA747	ABCA748	ABCA749	ABCA750	ABCA751	ABCA752	ABCA753	ABCA754	ABCA755	ABCA756	ABCA757	ABCA758	ABCA759	ABCA760	ABCA761	ABCA762	ABCA763	ABCA764	ABCA765	ABCA766	ABCA767	ABCA768	ABCA769	ABCA770	ABCA771	ABCA772	ABCA773	ABCA774	ABCA775	ABCA776	ABCA777	ABCA778	ABCA779	ABCA780	ABCA781	ABCA782	ABCA783	ABCA784	ABCA785	ABCA786	ABCA787	ABCA788	ABCA789	ABCA790	ABCA791	ABCA792	ABCA793	ABCA794	ABCA795	ABCA796	ABCA797	ABCA798	ABCA799	ABCA800	ABCA801	ABCA802	ABCA803	ABCA804	ABCA805	ABCA806	ABCA807	ABCA808	ABCA809	ABCA810	ABCA811	ABCA812	ABCA813	ABCA814	ABCA815	ABCA816	ABCA817	ABCA818	ABCA819	ABCA820	ABCA821	ABCA822	ABCA823	ABCA824	ABCA825	ABCA826	ABCA827	ABCA828	ABCA829	ABCA830	ABCA831	ABCA832	ABCA833	ABCA834	ABCA835	ABCA836	ABCA837	ABCA838	ABCA839	ABCA840	ABCA841	ABCA842	ABCA843	ABCA844	ABCA845	ABCA846	ABCA847	ABCA848	ABCA849	ABCA850	ABCA851	ABCA852	ABCA853	ABCA854	ABCA855	ABCA856	ABCA857	ABCA858	ABCA859	ABCA860	ABCA861	ABCA862	ABCA863	ABCA864	ABCA865	ABCA866	ABCA867	ABCA868	ABCA869	ABCA870	ABCA871	ABCA872	ABCA873	ABCA874	ABCA875	ABCA876	ABCA877	ABCA878	ABCA879	ABCA880	ABCA881	ABCA882	ABCA883	ABCA884	ABCA885	ABCA886	ABCA887	ABCA888	ABCA889	ABCA890	ABCA891	ABCA892	ABCA893	ABCA894	ABCA895	ABCA896	ABCA897	ABCA898	ABCA899	ABCA900	ABCA901	ABCA902	ABCA903	ABCA904	ABCA905	ABCA906	ABCA907	ABCA908	ABCA909	ABCA910	ABCA911	ABCA912	ABCA913	ABCA914	ABCA915	ABCA916	ABCA917	ABCA918	ABCA919	ABCA920	ABCA921	ABCA922	ABCA923	ABCA924	ABCA925	ABCA926	ABCA927	ABCA928	ABCA929	ABCA930	ABCA931	ABCA932	ABCA933	ABCA934	ABCA935	ABCA936	ABCA937	ABCA938	ABCA939	ABCA940	ABCA941	ABCA942	ABCA943	ABCA944	ABCA945	ABCA946	ABCA947	ABCA948	ABCA949	ABCA950	ABCA951	ABCA952	ABCA953	ABCA954	ABCA955	ABCA956	ABCA957	ABCA958	ABCA959	ABCA960	ABCA961	ABCA962	ABCA963	ABCA964	ABCA965	ABCA966	ABCA967	ABCA968	ABCA969	ABCA970	ABCA971	ABCA972	ABCA973	ABCA974	ABCA975	ABCA976	ABCA977	ABCA978	ABCA979	ABCA980	ABCA981	ABCA982	ABCA983	ABCA984	ABCA985	ABCA986	ABCA987	ABCA988	ABCA989	ABCA990	ABCA991	ABCA992	ABCA993	ABCA994	ABCA995	ABCA996	ABCA997	ABCA998	ABCA999	ABCA1000
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PEPCKE	ALLHDTIS	AD Virus (on bottom page)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500
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PROTEIN NAME	PROTEIN	ALL-INDIC	AB VEROCELL (see Bacteriophage 67)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6
POBATO VIRUS X (STRAIN C2) (PVX)	POBATO VIRUS X (STRAIN C2) (PVX)	110-147							
STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMVE)	STRAWBERRY MILD YELLOW EDGE-ASSOCIATED VIRUS (SMVE)	108-142							
WHITE CLOVER MOSAIC VIRUS (STRAIN M) (WCMV)	WHITE CLOVER MOSAIC VIRUS (STRAIN M) (WCMV)	1260-1289							
WHITE CLOVER MOSAIC VIRUS (STRAIN O) (WCMV)	WHITE CLOVER MOSAIC VIRUS (STRAIN O) (WCMV)	1260-1289							
AUTOGRAFIA CALIFORNICA NUCLEAR POLYOMEROSIS VIRUS (1)	AUTOGRAFIA CALIFORNICA NUCLEAR POLYOMEROSIS VIRUS (1)	1-41							
ONCHYIA PSEUDOTSUGATA MULTICAPSID POLYOMEROSIS VIRUS (1)	ONCHYIA PSEUDOTSUGATA MULTICAPSID POLYOMEROSIS VIRUS (1)	1-40							
RICE BLACK STREAKED DWARF VIRUS (RBSDV)	RICE BLACK STREAKED DWARF VIRUS (RBSDV)	175-372							
RICE GALL DWARF VIRUS (RGDV)	RICE GALL DWARF VIRUS (RGDV)	186-373							
WOUND TUMOR VIRUS (WTV)	WOUND TUMOR VIRUS (WTV)	273-314							
RICE DWARF VIRUS (RDV)	RICE DWARF VIRUS (RDV)	35-89							
WOUND TUMOR VIRUS (WTV)	WOUND TUMOR VIRUS (WTV)	16-74							
RICE DWARF VIRUS (RDV)	RICE DWARF VIRUS (RDV)	140-181							
WOUND TUMOR VIRUS (WTV)	WOUND TUMOR VIRUS (WTV)	64-108							
WOUND TUMOR VIRUS (WTV)	WOUND TUMOR VIRUS (WTV)	88-108							
LOUPOIN HERPESVIRUS TYPE 1 (STRAIN ADAP) (LHV-1)	LOUPOIN HERPESVIRUS TYPE 1 (STRAIN ADAP) (LHV-1)	186-373							
INDIAN CYTOMEGALOVIRUS (STRAIN ADAP)	INDIAN CYTOMEGALOVIRUS (STRAIN ADAP)	41-87							
HERPES SIMPLEX VIRUS (TYPE 6) (STRAIN UGANDA-1103)	HERPES SIMPLEX VIRUS (TYPE 6) (STRAIN UGANDA-1103)	174-371							
EBOLA VIRUS	EBOLA VIRUS	146-370							
EQUINE HERPESVIRUS TYPE 1 (STRAIN ADAP) (EHV-1)	EQUINE HERPESVIRUS TYPE 1 (STRAIN ADAP) (EHV-1)	38-77							
HERPESVIRUS SAIMIRI (STRAIN J1)	HERPESVIRUS SAIMIRI (STRAIN J1)	41-78							
ORGANIA PSEUDOTSUGATA MULTICAPSID POLYOMEROSIS VIRUS (1)	ORGANIA PSEUDOTSUGATA MULTICAPSID POLYOMEROSIS VIRUS (1)	116-119							
VARICELLA-ZOSTER VIRUS (STRAIN DUNAS) (VZV)	VARICELLA-ZOSTER VIRUS (STRAIN DUNAS) (VZV)	42-81							
AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4) (STRAIN VACC)	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4) (STRAIN VACC)	126-188							
BLUE TONGUE VIRUS (SEROTYPE 10) (ISOLATE USA)	BLUE TONGUE VIRUS (SEROTYPE 10) (ISOLATE USA)	168-235							
BLUE TONGUE VIRUS (SEROTYPE 11) (ISOLATE USA)	BLUE TONGUE VIRUS (SEROTYPE 11) (ISOLATE USA)	77-111							
BLUE TONGUE VIRUS (SEROTYPE 17) (ISOLATE USA)	BLUE TONGUE VIRUS (SEROTYPE 17) (ISOLATE USA)	77-111							
BLUE TONGUE VIRUS (SEROTYPE 17) (ISOLATE USA)	BLUE TONGUE VIRUS (SEROTYPE 17) (ISOLATE USA)	119-133							
EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1) (EHV)	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1) (EHV)	72-106							
BOVINE ROTAVIRUS (STRAIN M2)	BOVINE ROTAVIRUS (STRAIN M2)	5-94							
BOVINE ROTAVIRUS (STRAIN UK)	BOVINE ROTAVIRUS (STRAIN UK)	3-94							
HUMAN ROTAVIRUS (SEROTYPE 1) (STRAIN WA)	HUMAN ROTAVIRUS (SEROTYPE 1) (STRAIN WA)	17-87							
PORCINE ROTAVIRUS (GROUP C) (STRAIN COWDEN)	PORCINE ROTAVIRUS (GROUP C) (STRAIN COWDEN)	1-50							
SHUAN 11 ROTAVIRUS (STRAIN SAI)	SHUAN 11 ROTAVIRUS (STRAIN SAI)	16-94							
AFRICAN SWINE FEVER VIRUS (STRAIN E-75) (ASFV)	AFRICAN SWINE FEVER VIRUS (STRAIN E-75) (ASFV)	37-89							
FROG VIRUS 3 (FV3)	FROG VIRUS 3 (FV3)	37-81							
AFRICAN SWINE FEVER VIRUS (STRAIN BA1) (ASFV)	AFRICAN SWINE FEVER VIRUS (STRAIN BA1) (ASFV)	37-89							
EBOLA VIRUS	EBOLA VIRUS	80-119							
AUTOGRAFIA CALIFORNICA NUCLEAR POLYOMEROSIS VIRUS (1)	AUTOGRAFIA CALIFORNICA NUCLEAR POLYOMEROSIS VIRUS (1)	14-102							
BOVINE ROTAVIRUS (SEROTYPE 10) (ISOLATE USA)	BOVINE ROTAVIRUS (SEROTYPE 10) (ISOLATE USA)	16-102							
VACCINIA VIRUS (STRAIN COPELAND)	VACCINIA VIRUS (STRAIN COPELAND)	140-181							
VACCINIA VIRUS (STRAIN L-147)	VACCINIA VIRUS (STRAIN L-147)	17-31							
VACCINIA VIRUS (STRAIN W8)	VACCINIA VIRUS (STRAIN W8)	140-181							
VARICELLA VIRUS	VARICELLA VIRUS	141-182							
AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4) (STRAIN VACC)	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 4) (STRAIN VACC)	171-216							
BLUE TONGUE VIRUS (SEROTYPE 10) (ISOLATE USA)	BLUE TONGUE VIRUS (SEROTYPE 10) (ISOLATE USA)	116-235							
BLUE TONGUE VIRUS (SEROTYPE 17) (ISOLATE USA)	BLUE TONGUE VIRUS (SEROTYPE 17) (ISOLATE USA)	116-235							
BLUE T									

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[illegible]

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[illegible]

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FIGURE	ALL NOTIS	AN Virus (see Description)	AREA	AREA	AREA	AREA	AREA	AREA
FIGURE 1	ALL NOTIS							
FIGURE 2	ALL NOTIS							
FIGURE 3	ALL NOTIS							
FIGURE 4	ALL NOTIS							
FIGURE 5	ALL NOTIS							
FIGURE 6	ALL NOTIS							
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FIGURE 8	ALL NOTIS							
FIGURE 9	ALL NOTIS							
FIGURE 10	ALL NOTIS							
FIGURE 11	ALL NOTIS							
FIGURE 12	ALL NOTIS							
FIGURE 13	ALL NOTIS							
FIGURE 14	ALL NOTIS							
FIGURE 15	ALL NOTIS							
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FIGURE 18	ALL NOTIS							
FIGURE 19	ALL NOTIS							
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FIGURE 97	ALL NOTIS							
FIGURE 98	ALL NOTIS							
FIGURE 99	ALL NOTIS							
FIGURE 100	ALL NOTIS							

PCT/US 96/19495		All Viruses (see bacteriophage)									
ALL NOTIS											
PROTEIN											
PYVH VACC	PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9
PYVH VACC	HYPOTHETICAL 79 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	31-37								
PYVH VACC	HYPOTHETICAL 74 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	3-19								
PYVH VACC	HYPOTHETICAL 93 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	11-48								
PYVH VACC	HYPOTHETICAL 81 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	20-80								
PYVH VACC	HYPOTHETICAL 81 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	46-80								
PYVH VACC	HYPOTHETICAL 73 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	7-41								
PYVH VACC	HYPOTHETICAL 84 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	10-31								
PYVH VACC	HYPOTHETICAL 91 KD PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	9-31								

TABLE VI

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

108

GENE	ISOLATED	All Viruses (see bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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FCGID	1971-1974	1975-1979	1980-1984	1985-1989	1990-1994	1995-1999	2000-2004	2005-2009	2010-2014	2015-2019	2020-2024	2025-2029	2030-2034	2035-2039	2040-2044	2045-2049	2050-2054	2055-2059	2060-2064	2065-2069	2070-2074	2075-2079	2080-2084	2085-2089	2090-2094	2095-2099	2100-2104	2105-2109	2110-2114	2115-2119	2120-2124	2125-2129	2130-2134	2135-2139	2140-2144	2145-2149	2150-2154	2155-2159	2160-2164	2165-2169	2170-2174	2175-2179	2180-2184	2185-2189	2190-2194	2195-2199	2200-2204	2205-2209	2210-2214	2215-2219	2220-2224	2225-2229	2230-2234	2235-2239	2240-2244	2245-2249	2250-2254	2255-2259	2260-2264	2265-2269	2270-2274	2275-2279	2280-2284	2285-2289	2290-2294	2295-2299	2300-2304	2305-2309	2310-2314	2315-2319	2320-2324	2325-2329	2330-2334	2335-2339	2340-2344	2345-2349	2350-2354	2355-2359	2360-2364	2365-2369	2370-2374	2375-2379	2380-2384	2385-2389	2390-2394	2395-2399	2400-2404	2405-2409	2410-2414	2415-2419	2420-2424	2425-2429	2430-2434	2435-2439	2440-2444	2445-2449	2450-2454	2455-2459	2460-2464	2465-2469	2470-2474	2475-2479	2480-2484	2485-2489	2490-2494	2495-2499	2500-2504	2505-2509	2510-2514	2515-2519	2520-2524	2525-2529	2530-2534	2535-2539	2540-2544	2545-2549	2550-2554	2555-2559	2560-2564	2565-2569	2570-2574	2575-2579	2580-2584	2585-2589	2590-2594	2595-2599	2600-2604	2605-2609	2610-2614	2615-2619	2620-2624	2625-2629	2630-2634	2635-2639	2640-2644	2645-2649	2650-2654	2655-2659	2660-2664	2665-2669	2670-2674	2675-2679	2680-2684	2685-2689	2690-2694	2695-2699	2700-2704	2705-2709	2710-2714	2715-2719	2720-2724	2725-2729	2730-2734	2735-2739	2740-2744	2745-2749	2750-2754	2755-2759	2760-2764	2765-2769	2770-2774	2775-2779	2780-2784	2785-2789	2790-2794	2795-2799	2800-2804	2805-2809	2810-2814	2815-2819	2820-2824	2825-2829	2830-2834	2835-2839	2840-2844	2845-2849	2850-2854	2855-2859	2860-2864	2865-2869	2870-2874	2875-2879	2880-2884	2885-2889	2890-2894	2895-2899	2900-2904	2905-2909	2910-2914	2915-2919	2920-2924	2925-2929	2930-2934	2935-2939	2940-2944	2945-2949	2950-2954	2955-2959	2960-2964	2965-2969	2970-2974	2975-2979	2980-2984	2985-2989	2990-2994	2995-2999	3000-3004	3005-3009	3010-3014	3015-3019	3020-3024	3025-3029	3030-3034	3035-3039	3040-3044	3045-3049	3050-3054	3055-3059	3060-3064	3065-3069	3070-3074	3075-3079	3080-3084	3085-3089	3090-3094	3095-3099	3100-3104	3105-3109	3110-3114	3115-3119	3120-3124	3125-3129	3130-3134	3135-3139	3140-3144	3145-3149	3150-3154	3155-3159	3160-3164	3165-3169	3170-3174	3175-3179	3180-3184	3185-3189	3190-3194	3195-3199	3200-3204	3205-3209	3210-3214	3215-3219	3220-3224	3225-3229	3230-3234	3235-3239	3240-3244	3245-3249	3250-3254	3255-3259	3260-3264	3265-3269	3270-3274	3275-3279	3280-3284	3285-3289	3290-3294	3295-3299	3300-3304	3305-3309	3310-3314	3315-3319	3320-3324	3325-332
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[illegible]

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[illegible]

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PCGENE	1971-1984	1985-1990	1991-1995	1996-1999	2000-2003	2004-2007	2008-2011	2012-2015	2016-2019	2020-2023	2024-2027	2028-2031	2032-2035	2036-2039	2040-2043	2044-2047	2048-2051	2052-2055	2056-2059	2060-2063	2064-2067	2068-2071	2072-2075	2076-2079	2080-2083	2084-2087	2088-2091	2092-2095	2096-2099	2100-2103	2104-2107	2108-2111	2112-2115	2116-2119	2120-2123	2124-2127	2128-2131	2132-2135	2136-2139	2140-2143	2144-2147	2148-2151	2152-2155	2156-2159	2160-2163	2164-2167	2168-2171	2172-2175	2176-2179	2180-2183	2184-2187	2188-2191	2192-2195	2196-2199	2200-2203	2204-2207	2208-2211	2212-2215	2216-2219	2220-2223	2224-2227	2228-2231	2232-2235	2236-2239	2240-2243	2244-2247	2248-2251	2252-2255	2256-2259	2260-2263	2264-2267	2268-2271	2272-2275	2276-2279	2280-2283	2284-2287	2288-2291	2292-2295	2296-2299	2300-2303	2304-2307	2308-2311	2312-2315	2316-2319	2320-2323	2324-2327	2328-2331	2332-2335	2336-2339	2340-2343	2344-2347	2348-2351	2352-2355	2356-2359	2360-2363	2364-2367	2368-2371	2372-2375	2376-2379	2380-2383	2384-2387	2388-2391	2392-2395	2396-2399	2400-2403	2404-2407	2408-2411	2412-2415	2416-2419	2420-2423	2424-2427	2428-2431	2432-2435	2436-2439	2440-2443	2444-2447	2448-2451	2452-2455	2456-2459	2460-2463	2464-2467	2468-2471	2472-2475	2476-2479	2480-2483	2484-2487	2488-2491	2492-2495	2496-2499	2500-2503	2504-2507	2508-2511	2512-2515	2516-2519	2520-2523	2524-2527	2528-2531	2532-2535	2536-2539	2540-2543	2544-2547	2548-2551	2552-2555	2556-2559	2560-2563	2564-2567	2568-2571	2572-2575	2576-2579	2580-2583	2584-2587	2588-2591	2592-2595	2596-2599	2600-2603	2604-2607	2608-2611	2612-2615	2616-2619	2620-2623	2624-2627	2628-2631	2632-2635	2636-2639	2640-2643	2644-2647	2648-2651	2652-2655	2656-2659	2660-2663	2664-2667	2668-2671	2672-2675	2676-2679	2680-2683	2684-2687	2688-2691	2692-2695	2696-2699	2700-2703	2704-2707	2708-2711	2712-2715	2716-2719	2720-2723	2724-2727	2728-2731	2732-2735	2736-2739	2740-2743	2744-2747	2748-2751	2752-2755	2756-2759	2760-2763	2764-2767	2768-2771	2772-2775	2776-2779	2780-2783	2784-2787	2788-2791	2792-2795	2796-2799	2800-2803	2804-2807	2808-2811	2812-2815	2816-2819	2820-2823	2824-2827	2828-2831	2832-2835	2836-2839	2840-2843	2844-2847	2848-2851	2852-2855	2856-2859	2860-2863	2864-2867	2868-2871	2872-2875	2876-2879	2880-2883	2884-2887	2888-2891	2892-2895	2896-2899	2900-2903	2904-2907	2908-2911	2912-2915	2916-2919	2920-2923	2924-2927	2928-2931	2932-2935	2936-2939	2940-2943	2944-2947	2948-2951	2952-2955	2956-2959	2960-2963	2964-2967	2968-2971	2972-2975	2976-2979	2980-2983	2984-2987	2988-2991	2992-2995	2996-2999	3000-3003	3004-3007	3008-3011	3012-3015	3016-3019	3020-3023	3024-3027	3028-3031	3032-3035	3036-3039	3040-3043	3044-3047	3048-3051	3052-3055	3056-3059	3060-3063	3064-3067	3068-3071	3072-3075	3076-3079	3080-3083	3084-3087	3088-3091	3092-3095	3096-3099	3100-3103	3104-3107	3108-3111	3112-3115	3116-3119	3120-3123	3124-3127	3128-3131	3132-3135	3136-3139	3140-3143	3144-3147	
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PGENOME		180-178-4	AB Viruses (see Bacteriophage) (g)									
FILENAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	
PV0K TELVC	19 KD PROTEIN	TORACCO BATTLE VIRUS (STRAIN TCN1)	48-35									
PV0A DENV	2A PROTEIN	BROAD BEAM MOTTLE VIRUS	101-237									
PV0A COAV	2A PROTEIN	COWPEA CLOUTOTIC MOTTLE VIRUS	178-205									
PV0A CHVN	2A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FNY)	792-810									
PV0A EYI	2A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN J)	325-352	312-351								
PV0A TAV	2A PROTEIN	PEANUT STUNT VIRUS (STRAIN J)	313-360	322-356								
PV0K HCKVE	19 KD MAJOR EARLY PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN EBENHART)	194-221									
PV0K TELVC	30 KD PROTEIN	TORACCO BATTLE VIRUS (STRAIN TCN1)	130-160									
PV0P ABE41	31 KD PHOSPHOPROTEIN	HUMAN ADENOVIRUS TYPE 41	15-43									
PV0A ASB7	K143 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BA'IV)	35-102									
PV0A ASB7	G143 PROTEIN	AFRICAN SWINE FEVER VIRUS (STRAIN BA'IV)	3-30	173-199								
PV0A BAY	3A PROTEIN	BROME MOSAIC VIRUS	11-38									
PV0A CHVN	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN FSY)	222-232									
PV0A CHVM	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN M)	217-232									
PV0A QAVO	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN O)	222-231									
PV0A CHVY	3A PROTEIN	CUCUMBER MOSAIC VIRUS (STRAIN Y)	222-231									
PV0A BV8	3A PROTEIN	AVIAN INFECTIONOUS BRONCHITIS VIRUS (STRAIN HEALING-TTL)	25-57									
PV0A BV8	3A PROTEIN	AVIAN INFECTIONOUS BRONCHITIS VIRUS (STRAIN LK18 W66)	29-56									
PV0A BV8	3B PROTEIN	AVIAN INFECTIONOUS BRONCHITIS VIRUS (STRAIN BEAURETTE)	6-31									
PV0K BYDP	50 ED PROTEIN	SARLEY YELLOW DWAF VIRUS (ISOLATE PA'V)	119-146									
PV0E BWYV	11 ED PROTEIN	BEEF WESTERN YELLOW'S VIRUS (ISOLATE FL-1)	113-147	424-431								
PV0E BWYV	31 ED PROTEIN	BEEF WESTERN YELLOW'S VIRUS (ISOLATE GRI)	113-147	424-431								
PV0K PLV1	34 ED PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I)	124-131	418-472								
PV0K PLVW	34 ED PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	124-131	418-477								
PV0K PLVW	34 ED PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	124-131	418-477								
PV0K PLV1	49 ED PROTEIN	POTATO LEAFROLL VIRUS (STRAIN I)	110-160									
PV0K PLVW	49 ED PROTEIN	POTATO LEAFROLL VIRUS (STRAIN WAGENINGEN)	110-160									
PV0K AVYLE	90 ED PROTEIN	ALFA MOSAIC VIRUS (STRAIN A31 / ISOLATE LEIDEN)	107-134									
PV0K AVYLE	90 ED PROTEIN	ALFA MOSAIC VIRUS (STRAIN A31 / ISOLATE LEIDEN)	157-216	280-377	283-310	314-355						
PV0S VACC	PROTEIN A2	VACCINIA VIRUS (STRAIN COPENHAGEN)	156-215	249-276	282-309	312-354						
PV0S VACC	PROTEIN A3	VACCINIA VIRUS (STRAIN WR)	157-216	256-277	283-310	314-355						
PV0S VACC	PROTEIN A4	VACCINIA VIRUS (STRAIN COPENHAGEN)	176-206									
PV0S VACC	PROTEIN A5	VACCINIA VIRUS (STRAIN COPENHAGEN)	176-206									
PV0S VACC	PROTEIN A6	VACCINIA VIRUS (STRAIN COPENHAGEN)	60-93									
PV0S VACC	PROTEIN A7	VACCINIA VIRUS (STRAIN COPENHAGEN)	219-283									
PV0S VACC	PROTEIN A8	VACCINIA VIRUS (STRAIN COPENHAGEN)	280-284									
PV0S VACC	PROTEIN A9	VACCINIA VIRUS (STRAIN COPENHAGEN)	400-467									
PV0S VACC	PROTEIN A10	VACCINIA VIRUS (STRAIN COPENHAGEN)	4-67	310-337								
PV0S VACC	PROTEIN A11	VACCINIA VIRUS (STRAIN COPENHAGEN)	8-47	310-337								
PV0S VACC	PROTEIN A12	VACCINIA VIRUS (STRAIN COPENHAGEN)	41-72									
PV0S VACC	PROTEIN A13	VACCINIA VIRUS (STRAIN COPENHAGEN)	91-144									
PV0S VACC	PROTEIN A14	VACCINIA VIRUS (STRAIN COPENHAGEN)	95-144									
PV0S VACC	PROTEIN A15	VACCINIA VIRUS (STRAIN WR)	22-49									
PV0S VACC	PROTEIN A16	VACCINIA VIRUS (STRAIN WR)	22-49									
PV0S VACC	PROTEIN A17	VACCINIA VIRUS (STRAIN WR)	12-55									
PV0S VACC	PROTEIN A18	VACCINIA VIRUS (STRAIN COPENHAGEN)	88-115									
PV0S VACC	PROTEIN A19	VACCINIA VIRUS (STRAIN COPENHAGEN)	88-115									
PV0S VACC	PROTEIN A20	VACCINIA VIRUS (STRAIN COPENHAGEN)	88-122									
PV0S VACC	PROTEIN A21	VACCINIA VIRUS (STRAIN COPENHAGEN)	87-114									
PV0S VACC	PROTEIN A22	VACCINIA VIRUS (STRAIN COPENHAGEN)	87-114									
PV0S VACC	PROTEIN A23	VACCINIA VIRUS (STRAIN WR)	97-114									
PV0S VACC	PROTEIN A24	VACCINIA VIRUS (STRAIN WR)	97-114									
PV0S VACC	PROTEIN A25	VACCINIA VIRUS (STRAIN WR)	120-155									
PV0S VACC	PROTEIN A26	VACCINIA VIRUS (STRAIN WR)	120-155									
PV0S VACC	PROTEIN A27	VACCINIA VIRUS (STRAIN COPENHAGEN)	127-154									
PV0S VACC	PROTEIN A28	VACCINIA VIRUS (STRAIN COPENHAGEN)	127-154									
PV0S VACC	PROTEIN A29	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A30	VACCINIA VIRUS (STRAIN WR)	44-81									
PV0S VACC	PROTEIN A31	VACCINIA VIRUS (STRAIN WR)	44-81									
PV0S VACC	PROTEIN A32	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A33	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A34	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A35	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A36	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A37	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A38	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A39	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A40	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A41	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A42	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A43	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A44	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A45	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A46	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A47	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A48	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A49	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A50	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A51	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A52	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A53	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A54	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A55	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A56	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A57	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A58	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A59	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A60	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A61	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A62	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A63	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A64	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A65	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A66	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A67	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A68	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A69	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A70	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A71	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A72	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A73	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A74	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A75	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A76	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A77	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A78	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A79	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A80	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A81	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A82	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A83	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A84	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A85	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A86	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A87	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A88	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A89	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A90	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A91	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A92	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A93	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A94	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A95	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A96	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A97	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A98	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A99	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A100	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A101	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A102	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A103	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A104	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A105	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A106	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A107	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A108	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A109	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A110	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A111	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A112	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A113	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A114	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-81									
PV0S VACC	PROTEIN A115	VACCINIA VIRUS (STRAIN COPENHAGEN)										

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[illegible]

GENE	10/1/14	ALL Viruses (see Description pages)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500	AREA 501	AREA 502	AREA 503	AREA 504	AREA 505	AREA 506	AREA 507	AREA 508	AREA 509	AREA 510	AREA 511	AREA 512	AREA 513	AREA 514	AREA 515	AREA 516	AREA 517	AREA 518	AREA 519	AREA 520	AREA 521	AREA 522	AREA 523	AREA 524	AREA 525	AREA 526	AREA 527	AREA 528	AREA 529	AREA 530	AREA 531	AREA 532	AREA 533	AREA 534	AREA 535	AREA 536	AREA 537	AREA 538	AREA 539	AREA 540	AREA 541	AREA 542	AREA 543	AREA 544	AREA 545	AREA 546	AREA 547	AREA 548	AREA 549	AREA 550	AREA 551	AREA 552	AREA 553	AREA 554	AREA 555	AREA 556	AREA 557	AREA 558	AREA 559	AREA 560	AREA 561	AREA 562	AREA 563	AREA 564	AREA 565	AREA 566	AREA 567	AREA 568	AREA 569	AREA 570	AREA 571	AREA 572	AREA 573	AREA 574	AREA 575	AREA 576	AREA 577	AREA 578	AREA 579	AREA 580	AREA 581	AREA 582	AREA 583	AREA 584	AREA 585	AREA 586	AREA 587	AREA 588	AREA 589	AREA 590	AREA 591	AREA 592	AREA 593	AREA 594	AREA 595	AREA 596	AREA 597	AREA 598	AREA 599	AREA 600	AREA 601	AREA 602	AREA 603	AREA 604	AREA 605	AREA 606	AREA 607	AREA 608	AREA 609	AREA 610	AREA 611	AREA 612	AREA 613	AREA 614	AREA 615	AREA 616	AREA 617	AREA 618	AREA 619	AREA 620	AREA 621	AREA 622	AREA 623	AREA 624	AREA 625	AREA 626	AREA 627	AREA 628	AREA 629	AREA 630	AREA 631	AREA 632	AREA 633	AREA 634	AREA 635	AREA 636	AREA 637	AREA 638	AREA 639	AREA 640	AREA 641	AREA 642	AREA 643	AREA 644	AREA 645	AREA 646	AREA 647	AREA 648	AREA 649	AREA 650	AREA 651	AREA 652	AREA 653	AREA 654	AREA 655	AREA 656	AREA 657	AREA 658	AREA 659	AREA 660	AREA 661	AREA 662	AREA 663	AREA 664	AREA 665	AREA 666	AREA 667	AREA 668	AREA 669	AREA 670	AREA 671	AREA 672	AREA 673	AREA 674	AREA 675	AREA 676	AREA 677	AREA 678	AREA 679	AREA 680	AREA 681	AREA 682	AREA 683	AREA 684	AREA 685	AREA 686	AREA 687	AREA 688	AREA 689	AREA 690	AREA 691	AREA 692	AREA 693	AREA 694	AREA 695	AREA 696	AREA 697	AREA 698	AREA 699	AREA 700	AREA 701	AREA 702	AREA 703	AREA 704	AREA 705	AREA 706	AREA 707	AREA 708	AREA 709	AREA 710	AREA 711	AREA 712	AREA 713	AREA 714	AREA 715	AREA 716	AREA 717	AREA 718	AREA 719	AREA 720	AREA 721	AREA 722	AREA 723	AREA 724	AREA 725	AREA 726	AREA 727	AREA 728	AREA 729	AREA 730	AREA 731	AREA 732	AREA 733	AREA 734	AREA 735	AREA 736	AREA 737	AREA 738	AREA 739	AREA 740	AREA 741	AREA 742	AREA 743	AREA 744	AREA 745	AREA 746	AREA 747	AREA 748	AREA 749	AREA 750	AREA 751	AREA 752	AREA 753	AREA 754	AREA 755	AREA 756	AREA 757	AREA 758	AREA 759	AREA 760	AREA 761	AREA 762	AREA 763	AREA 764	AREA 765	AREA 766	AREA 767	AREA 768	AREA 769	AREA 770	AREA 771	AREA 772	AREA 773	AREA 774	AREA 775	AREA 776	AREA 777	AREA 778	AREA 779	AREA 780	AREA 781	AREA 782	AREA 783	AREA 784	AREA 785	AREA 786	AREA 787	AREA 788	AREA 789	AREA 790	AREA 791	AREA 792	AREA 793	AREA 794	AREA 795	AREA 796	AREA 797	AREA 798	AREA 799	AREA 800	AREA 801	AREA 802	AREA 803	AREA 804	AREA 805	AREA 806	AREA 807	AREA 808	AREA 809	AREA 810	AREA 811	AREA 812	AREA 813	AREA 814	AREA 815	AREA 816	AREA 817	AREA 818	AREA 819	AREA 820	AREA 821	AREA 822	AREA 823	AREA 824	AREA 825	AREA 826	AREA 827	AREA 828	AREA 829	AREA 830	AREA 831	AREA 832	AREA 833	AREA 834	AREA 835	AREA 836	AREA 837	AREA 838	AREA 839	AREA 840	AREA 841	AREA 842	AREA 843	AREA 844	AREA 845	AREA 846	AREA 847	AREA 848	AREA 849	AREA 850	AREA 851	AREA 852	AREA 853	AREA 854	AREA 855	AREA 856	AREA 857	AREA 858	AREA 859	AREA 860	AREA 861	AREA 862	AREA 863	AREA 864	AREA 865	AREA 866	AREA 867	AREA 868	AREA 869	AREA 870	AREA 871	AREA 872	AREA 873	AREA 874	AREA 875	AREA 876	AREA 877	AREA 878	AREA 879	AREA 880	AREA 881	AREA 882	AREA 883	AREA 884	AREA 885	AREA 886	AREA 887	AREA 888	AREA 889	AREA 890	AREA 891	AREA 892	AREA 893	AREA 894	AREA 895	AREA 896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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PGENE	INITIAL	ALL Variants (see Background)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
IL28RA1	PROTEIN	VIRUS									
PV01 HSVB	GENE 1 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN AIRHP)	146-176								
PV02 HSVB	GENE 3 PROTEIN	EQUINE HERPESVIRUS TYPE 1 (STRAIN KENTIAU NYA)	146-176								
PV03 VACC	PROTEIN G1	VACCINIA VIRUS (STRAIN COPENHAGEN)	44-75	131-161	235-289	335-389					
PV04 VAR	PROTEIN G3	VARIOLA VIRUS	44-75	124-161	235-289	335-389					
PV05 HSVI	HYPOH GENE 1 MEDAB PRO	ICTALURID HERPESVIRUS 1	71-98								
PV06 VACC	PROTEIN F1	VACCINIA VIRUS (STRAIN COPENHAGEN)	308-318								
PV07 VACC	PROTEIN F1	VACCINIA VIRUS (STRAIN NY)	371-381								
PV08 VAR	PROTEIN F1	VARIOLA VIRUS	308-318								
PV09 HSVI	GENE 11 PROTEIN	SPIROPLASMA VIRUS SPV1-RIA2 B	11-45								
PV10 HSVI	HYPOHETICAL GENE 13 PROTEIN	ICTALURID HERPESVIRUS 1	177-204								
PV11 HSVI	HYPOHETICAL GENE 13 PROTEIN	ICTALURID HERPESVIRUS 1	174-208								
PV12 HSVI	HYPOHETICAL GENE 13 PROTEIN	ICTALURID HERPESVIRUS 1	365-387								
PV13 SPV4	CAPSID PROTEIN	SPIROPLASMA VIRUS SPV1-RIA2 B	287-314	181-410	668-703	766-824					
PV14 HSVI	HYPOHETICAL GENE 23 PROTEIN	ICTALURID HERPESVIRUS 1	375-400	581-632							
PV15 HSVI	HYPOHETICAL GENE 24 PROTEIN	ICTALURID HERPESVIRUS 1	31-38	497-528							
PV16 HSVI	HYPOHETICAL GENE 25 PROTEIN	ICTALURID HERPESVIRUS 1	235-300								
PV17 HSVI	HYPOHETICAL GENE 25 PROTEIN	ICTALURID HERPESVIRUS 1	31-64	91-118							
PV18 AMEPV	HYPOHETICAL GIL PROTEIN	AMSACTA MOOREI ENTOMOPHOXVIRUS	283-320								
PV19 SPV4	GENE 3 PROTEIN	SPIROPLASMA VIRUS SPV1-RIA2 B	146-173	175-205	262-310						
PV20 HSVI	HYPOHETICAL GENE 24 PROTEIN	ICTALURID HERPESVIRUS 1	95-122								
PV21 HSVI	HYPOHETICAL GENE 31 PROTEIN	ICTALURID HERPESVIRUS 1	442-469								
PV22 HSVI	HYPOHETICAL GENE 31 PROTEIN	ICTALURID HERPESVIRUS 1	531-678	1088-1115							
PV23 AMEPV	HYPOHETICAL GIL PROTEIN	AMSACTA MOOREI ENTOMOPHOXVIRUS	2-29								
PV24 HSVI	GENE 3 PROTEIN	SPIROPLASMA VIRUS SPV1-RIA2 B	15-49								
PV25 HSVI	HYPOHETICAL GENE 21 PROTEIN	ICTALURID HERPESVIRUS 1	18-32	87-148							
PV26 HSVI	HYPOHETICAL GENE 21 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	118-163								
PV27 HSVI	PROBABLE MAJOR GLYCOPROTEIN	ICTALURID HERPESVIRUS 1	142-169	346-371	897-924	913-1007					
PV28 HSVI	PROBABLE MAJOR GLYCOPROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	365-394								
PV29 AMEPV	QAR PROTEIN	AMSACTA MOOREI ENTOMOPHOXVIRUS	4-31								
PV30 SPV4	GENE 4 PROTEIN	SPIROPLASMA VIRUS SPV1-RIA2 B	116-146								
PV31 HSVI	HYPOH GENE 51 MEMBRANE PROTEIN	ICTALURID HERPESVIRUS 1	34-61	87-114							
PV32 HSVI	HYPOHETICAL GENE 51 PROTEIN	HERPESVIRUS SAIMIRI (STRAIN 11)	47-74								
PV33 HSVI	HYPOHETICAL GENE 54 PROTEIN	ICTALURID HERPESVIRUS 1	382-609								
PV34 SPV4	GENE 5 PROTEIN	SPIROPLASMA VIRUS SPV1-RIA2 B	65-93								
PV35 HSVI	HYPOHETICAL GENE 63 PROTEIN	ICTALURID HERPESVIRUS 1	36-43								
PV36 HSVI	HYPOHETICAL GENE 64 PROTEIN	ICTALURID HERPESVIRUS 1	550-584								
PV37 HSVI	HYPOHETICAL GENE 65 PROTEIN	ICTALURID HERPESVIRUS 1	477-504								
PV38 HSVI	HYPOHETICAL GENE 65 PROTEIN	ICTALURID HERPESVIRUS 1	1213-1234								
PV39 HSVI	HYPOHETICAL GENE 66 PROTEIN	ICTALURID HERPESVIRUS 1	382-408								
PV40 HSVI	HYPOHETICAL GENE 67 PROTEIN	ICTALURID HERPESVIRUS 1	1342-1369								
PV41 HSVI	HYPOHETICAL GENE 68 PROTEIN	ICTALURID HERPESVIRUS 1	281-288								
PV42 HSVI	HYPOHETICAL GENE 72 PROTEIN	ICTALURID HERPESVIRUS 1	447-481								
PV43 HSVI	HYPOHETICAL GENE 73 PROTEIN	ICTALURID HERPESVIRUS 1	388-432								
PV44 HSVI	HYPOHETICAL GENE 74 PROTEIN	ICTALURID HERPESVIRUS 1	388-432								
PV45 SPV4	GENE 7 PROTEIN	SPIROPLASMA VIRUS 4	388-432								
PV46 HSVI	HYPOHETICAL GENE 74 PROTEIN	ICTALURID HERPESVIRUS 1	14-44								
PV47 HSVI	HYPOHETICAL GENE 74 PROTEIN	AVIAN INFECTIONOUS BROMCHITIS VIRUS	1210-1260	2408-2433							
PV48 HSVI	HYPOHETICAL GENE 74 PROTEIN	BOVINE CORONA VIRUS (STRAIN F15)	398-428	642-676	1023-1064	1278-1301					
PV49 HSVI	HYPOHETICAL GENE 74 PROTEIN	BOVINE CORONA VIRUS (STRAIN L9)	398-428	642-676	1023-1064	1278-1301					
PV50 HSVI	HYPOHETICAL GENE 74 PROTEIN	BOVINE CORONA VIRUS (STRAIN L V J3)	398-428	642-676	1023-1064	1278-1301					
PV51 HSVI	HYPOHETICAL GENE 74 PROTEIN	BOVINE CORONA VIRUS (STRAIN NEBUS)	398-428	642-676	1023-1064	1278-1301					
PV52 HSVI	HYPOHETICAL GENE 74 PROTEIN	BOVINE CORONA VIRUS (STRAIN QUEBEC)	398-428	642-676	1023-1064	1278-1301					
PV53 HSVI	HYPOHETICAL GENE 74 PROTEIN	BOVINE CORONA VIRUS (STRAIN VACCINE)	398-428	642-676	1023-1064	1278-1301					
PV54 HSVI	HYPOHETICAL GENE 74 PROTEIN	HUMAN CORONA VIRUS (STRAIN 229E)	716-797	809-873	1054-1113						
PV55 HSVI	HYPOHETICAL GENE 74 PROTEIN	HUMAN CORONA VIRUS (STRAIN WILD TYPE 1)	441-484	1010-1092							
PV56 HSVI	HYPOHETICAL GENE 74 PROTEIN	HUMAN CORONA VIRUS (STRAIN A19)	34-63	591-632	978-1040						
PV57 HSVI	HYPOHETICAL GENE 74 PROTEIN	HUMAN CORONA VIRUS (STRAIN H19)	642-684	1010-1092							
PV58 HSVI	HYPOHETICAL GENE 74 PROTEIN	HUMAN CORONA VIRUS (STRAIN H19)	902-943	189-911							

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PCGENE	10/17/84	ALL Viruses (not bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																

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PCGENE	10131844	ALL Viruses (see bacteriophage)	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
FILE NAME	PROTEIN	VIRUS	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9
PV01 ROTAV	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN C486)	595-439	594-427							
PV02 ROTAV	OUTER CAPSID PROTEIN VP4	BOVINE ROTAVIRUS (STRAIN C486)	595-439	594-427							
PV03 ROTAV	OUTER CAPSID PROTEIN VP4	EQUINE ROTAVIRUS (STRAIN H-2)	595-439	594-427							
PV04 ROTAV	OUTER CAPSID PROTEIN VP4	ROTAVIRUS (GROUP B / STRAIN IDH)	595-439	594-427							
PV05 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 1076)	595-439	594-427							
PV06 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN RV-3)	595-439	594-427							
PV07 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN 694)	595-439	594-427							
PV08 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN 1071)	595-439	594-427							
PV09 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN K4)	595-439	594-427							
PV10 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN KU)	595-439	594-427							
PV11 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (STRAIN L36)	595-439	594-427							
PV12 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN M17)	595-439	594-427							
PV13 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN MCN1)	595-439	594-427							
PV14 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN P)	595-439	594-427							
PV15 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN RV)	595-439	594-427							
PV16 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3)	595-439	594-427							
PV17 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN VA 9)	595-439	594-427							
PV18 ROTAV	OUTER CAPSID PROTEIN VP4	HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN WA)	595-439	594-427							
PV19 ROTAV	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (SEROTYPE 3 / STRAIN OSU)	595-439	594-427							
PV20 ROTAV	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (GROUP C / STRAIN COMDEN)	595-439	594-427							
PV21 ROTAV	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN GOTTFRIED)	595-439	594-427							
PV22 ROTAV	OUTER CAPSID PROTEIN VP4	PORCINE ROTAVIRUS (STRAIN YAG)	595-439	594-427							
PV23 ROTAV	OUTER CAPSID PROTEIN VP4	RHESUS ROTAVIRUS	595-439	594-427							
PV24 ROTAV	OUTER CAPSID PROTEIN VP4	SIMIAN 11 ROTAVIRUS (STRAIN SA11-HEM)	595-439	594-427							
PV25 ROTAV	OUTER CAPSID PROTEIN VP4	SIMIAN 11 ROTAVIRUS (STRAIN SA11-SEM)	595-439	594-427							
PV26 ROTAV	OUTER CAPSID PROTEIN VP4	WOUND TUMOR VIRUS	595-439	594-427							
PV27 ROTAV	MONOSTRUCTURAL PROTEIN PMS4	WOUND TUMOR VIRUS	595-439	594-427							
PV28 ROTAV	OUTER CAPSID PROTEIN VP5	AFRICAN HORSE SICKNESS VIRUS (SEROTYPE 1 / STRAIN VACCINE)	595-439	594-427							
PV29 ROTAV	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	595-439	594-427							
PV30 ROTAV	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	595-439	594-427							
PV31 ROTAV	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)	595-439	594-427							
PV32 ROTAV	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	595-439	594-427							
PV33 ROTAV	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE AUSTRALIA)	595-439	594-427							
PV34 ROTAV	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE SOUTH AFRICA)	595-439	594-427							
PV35 ROTAV	OUTER CAPSID PROTEIN VP5	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	595-439	594-427							
PV36 ROTAV	OUTER CAPSID PROTEIN VP5	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	595-439	594-427							
PV37 ROTAV	OUTER COAT PROTEIN P5	WOUND TUMOR VIRUS	595-439	594-427							
PV38 ROTAV	VP5 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	595-439	594-427							
PV39 ROTAV	PROB. MONOSTRUCT. 41.0 ED PRO	MAIZE RACHIS DWARF VIRUS	595-439	594-427							
PV40 ROTAV	41 ED PROTEIN	AUTOCORONA CALIFORNICA NUCLEAR POLYOMEROSIS VIRUS	595-439	594-427							
PV41 ROTAV	VP5 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	595-439	594-427							
PV42 ROTAV	MAJOR ENV GLYCOPROTEIN PRECURSOR	ORITIA PSEUDOTUBERCULATA MULTICAPSID POLYOMEROSIS VIRUS	595-439	594-427							
PV43 ROTAV	VP4 PROTEIN	AUTOCORONA CALIFORNICA NUCLEAR POLYOMEROSIS VIRUS	595-439	594-427							
PV44 ROTAV	VP4 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 11 / ISOLATE USA)	595-439	594-427							
PV45 ROTAV	VP4 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)	595-439	594-427							
PV46 ROTAV	VP4 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 17 / ISOLATE USA)	595-439	594-427							
PV47 ROTAV	VP4 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 1 / ISOLATE SOUTH AFRICA)	595-439	594-427							
PV48 ROTAV	VP4 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 2 / ISOLATE USA)	595-439	594-427							
PV49 ROTAV	STRUCTURAL PROTEIN P4	RICE DWARF VIRUS	595-439	594-427							
PV50 ROTAV	P4 PROTEIN	AUTOCORONA CALIFORNICA NUCLEAR POLYOMEROSIS VIRUS	595-439	594-427							
PV51 ROTAV	PROBABLE MEMBRANE ANTIGEN 15	HEPES VIRUS (STRAIN 11)	595-439	594-427							
PV52 ROTAV	VP7 CORE PROTEIN	AUTOCORONA CALIFORNICA NUCLEAR POLYOMEROSIS VIRUS	595-439	594-427							
PV53 ROTAV	VP7 CORE PROTEIN	EPIDEMIC HEMORRHAGIC DISEASE VIRUS (SEROTYPE 1)	595-439	594-427							
PV54 ROTAV	NONSTRUCTURAL PROTEIN PMS7	WOUND TUMOR VIRUS	595-439	594-427							
PV55 ROTAV	CAPSID PROTEIN P6	AUTOCORONA CALIFORNICA NUCLEAR POLYOMEROSIS VIRUS	595-439	594-427							
PV56 ROTAV	CAPSID PROTEIN P7	ORITIA PSEUDOTUBERCULATA MULTICAPSID POLYOMEROSIS VIRUS	595-439	594-427							
PV57 ROTAV	STRUCTURAL PROTEIN P8	BLUETONGUE VIRUS (SEROTYPE 10 / ISOLATE USA)	595-439	594-427							
PV58 ROTAV	STRUCTURAL PROTEIN VP8 PRECURSOR	FOWLPOX VIRUS	595-439	594-427							

Accession	Gene	Protein	Strain	Area 1	Area 2	Area 3	Area 4	Area 5	Area 6	Area 7	Area 8	Area 9	Area 10	Area 11	Area 12	Area 13	Area 14	Area 15	Area 16	Area 17	Area 18	Area 19	Area 20	Area 21	Area 22	Area 23	Area 24	Area 25	Area 26	Area 27	Area 28	Area 29	Area 30	Area 31	Area 32	Area 33	Area 34	Area 35	Area 36	Area 37	Area 38	Area 39	Area 40	Area 41	Area 42	Area 43	Area 44	Area 45	Area 46	Area 47	Area 48	Area 49	Area 50	Area 51	Area 52	Area 53	Area 54	Area 55	Area 56	Area 57	Area 58	Area 59	Area 60	Area 61	Area 62	Area 63	Area 64	Area 65	Area 66	Area 67	Area 68	Area 69	Area 70	Area 71	Area 72	Area 73	Area 74	Area 75	Area 76	Area 77	Area 78	Area 79	Area 80	Area 81	Area 82	Area 83	Area 84	Area 85	Area 86	Area 87	Area 88	Area 89	Area 90	Area 91	Area 92	Area 93	Area 94	Area 95	Area 96	Area 97	Area 98	Area 99	Area 100	Area 101	Area 102	Area 103	Area 104	Area 105	Area 106	Area 107	Area 108	Area 109	Area 110	Area 111	Area 112	Area 113	Area 114	Area 115	Area 116	Area 117	Area 118	Area 119	Area 120	Area 121	Area 122	Area 123	Area 124	Area 125	Area 126	Area 127	Area 128	Area 129	Area 130	Area 131	Area 132	Area 133	Area 134	Area 135	Area 136	Area 137	Area 138	Area 139	Area 140	Area 141	Area 142	Area 143	Area 144	Area 145	Area 146	Area 147	Area 148	Area 149	Area 150	Area 151	Area 152	Area 153	Area 154	Area 155	Area 156	Area 157	Area 158	Area 159	Area 160	Area 161	Area 162	Area 163	Area 164	Area 165	Area 166	Area 167	Area 168	Area 169	Area 170	Area 171	Area 172	Area 173	Area 174	Area 175	Area 176	Area 177	Area 178	Area 179	Area 180	Area 181	Area 182	Area 183	Area 184	Area 185	Area 186	Area 187	Area 188	Area 189	Area 190	Area 191	Area 192	Area 193	Area 194	Area 195	Area 196	Area 197	Area 198	Area 199	Area 200	Area 201	Area 202	Area 203	Area 204	Area 205	Area 206	Area 207	Area 208	Area 209	Area 210	Area 211	Area 212	Area 213	Area 214	Area 215	Area 216	Area 217	Area 218	Area 219	Area 220	Area 221	Area 222	Area 223	Area 224	Area 225	Area 226	Area 227	Area 228	Area 229	Area 230	Area 231	Area 232	Area 233	Area 234	Area 235	Area 236	Area 237	Area 238	Area 239	Area 240	Area 241	Area 242	Area 243	Area 244	Area 245	Area 246	Area 247	Area 248	Area 249	Area 250	Area 251	Area 252	Area 253	Area 254	Area 255	Area 256	Area 257	Area 258	Area 259	Area 260	Area 261	Area 262	Area 263	Area 264	Area 265	Area 266	Area 267	Area 268	Area 269	Area 270	Area 271	Area 272	Area 273	Area 274	Area 275	Area 276	Area 277	Area 278	Area 279	Area 280	Area 281	Area 282	Area 283	Area 284	Area 285	Area 286	Area 287	Area 288	Area 289	Area 290	Area 291	Area 292	Area 293	Area 294	Area 295	Area 296	Area 297	Area 298	Area 299	Area 300	Area 301	Area 302	Area 303	Area 304	Area 305	Area 306	Area 307	Area 308	Area 309	Area 310	Area 311	Area 312	Area 313	Area 314	Area 315	Area 316	Area 317	Area 318	Area 319	Area 320	Area 321	Area 322	Area 323	Area 324	Area 325	Area 326	Area 327	Area 328	Area 329	Area 330	Area 331	Area 332	Area 333	Area 334	Area 335	Area 336	Area 337	Area 338	Area 339	Area 340	Area 341	Area 342	Area 343	Area 344	Area 345	Area 346	Area 347	Area 348	Area 349	Area 350	Area 351	Area 352	Area 353	Area 354	Area 355	Area 356	Area 357	Area 358	Area 359	Area 360	Area 361	Area 362	Area 363	Area 364	Area 365	Area 366	Area 367	Area 368	Area 369	Area 370	Area 371	Area 372	Area 373	Area 374	Area 375	Area 376	Area 377	Area 378	Area 379	Area 380	Area 381	Area 382	Area 383	Area 384	Area 385	Area 386	Area 387	Area 388	Area 389	Area 390	Area 391	Area 392	Area 393	Area 394	Area 395	Area 396	Area 397	Area 398	Area 399	Area 400	Area 401	Area 402	Area 403	Area 404	Area 405	Area 406	Area 407	Area 408	Area 409	Area 410	Area 411	Area 412	Area 413	Area 414	Area 415	Area 416	Area 417	Area 418	Area 419	Area 420	Area 421	Area 422	Area 423	Area 424	Area 425	Area 426	Area 427	Area 428	Area 429	Area 430	Area 431	Area 432	Area 433	Area 434	Area 435	Area 436	Area 437	Area 438	Area 439	Area 440	Area 441	Area 442	Area 443	Area 444	Area 445	Area 446	Area 447	Area 448	Area 449	Area 450	Area 451	Area 452	Area 453	Area 454	Area 455	Area 456	Area 457	Area 458	Area 459	Area 460	Area 461	Area 462	Area 463	Area 464	Area 465	Area 466	Area 467	Area 468	Area 469	Area 470	Area 471	Area 472	Area 473	Area 474	Area 475	Area 476	Area 477	Area 478	Area 479	Area 480	Area 481	Area 482	Area 483	Area 484	Area 485	Area 486	Area 487	Area 488	Area 489	Area 490	Area 491	Area 492	Area 493	Area 494	Area 495	Area 496	Area 497	Area 498	Area 499	Area 500	Area 501	Area 502	Area 503	Area 504	Area 505	Area 506	Area 507	Area 508	Area 509	Area 510	Area 511	Area 512	Area 513	Area 514	Area 515	Area 516	Area 517	Area 518	Area 519	Area 520	Area 521	Area 522	Area 523	Area 524	Area 525	Area 526	Area 527	Area 528	Area 529	Area 530	Area 531	Area 532	Area 533	Area 534	Area 535	Area 536	Area 537	Area 538	Area 539	Area 540	Area 541	Area 542	Area 543	Area 544	Area 545	Area 546	Area 547	Area 548	Area 549	Area 550	Area 551	Area 552	Area 553	Area 554	Area 555	Area 556	Area 557	Area 558	Area 559	Area 560	Area 561	Area 562	Area 563	Area 564	Area 565	Area 566	Area 567	Area 568	Area 569	Area 570	Area 571	Area 572	Area 573	Area 574	Area 575	Area 576	Area 577	Area 578	Area 579	Area 580	Area 581	Area 582	Area 583	Area 584	Area 585	Area 586	Area 587	Area 588	Area 589	Area 590	Area 591	Area 592	Area 593	Area 594	Area 595	Area 596	Area 597	Area 598	Area 599	Area 600	Area 601	Area 602	Area 603	Area 604	Area 605	Area 606	Area 607	Area 608	Area 609	Area 610	Area 611	Area 612	Area 613	Area 614	Area 615	Area 616	Area 617	Area 618	Area 619	Area 620	Area 621	Area 622	Area 623	Area 624	Area 625	Area 626	Area 627	Area 628	Area 629	Area 630	Area 631	Area 632	Area 633	Area 634	Area 635	Area 636	Area 637	Area 638	Area 639	Area 640	Area 641	Area 642	Area 643	Area 644	Area 645	Area 646	Area 647	Area 648	Area 649	Area 650	Area 651	Area 652	Area 653	Area 654	Area 655	Area 656	Area 657	Area 658	Area 659	Area 660	Area 661	Area 662	Area 663	Area 664	Area 665	Area 666	Area 667	Area 668	Area 669	Area 670	Area 671	Area 672	Area 673	Area 674	Area 675	Area 676	Area 677	Area 678	Area 679	Area 680	Area 681	Area 682	Area 683	Area 684	Area 685	Area 686	Area 687	Area 688	Area 689	Area 690	Area 691	Area 692	Area 693	Area 694	Area 695	Area 696	Area 697	Area 698	Area 699	Area 700	Area 701	Area 702	Area 703	Area 704	Area 705	Area 706	Area 707	Area 708	Area 709	Area 710	Area 711	Area 712	Area 713	Area 714	Area 715	Area 716	Area 717	Area 718	Area 719	Area 720	Area 721	Area 722	Area 723	Area 724	Area 725	Area 726	Area 727	Area 728	Area 729	Area 730	Area 731	Area 732	Area 733	Area 734	Area 735	Area 736	Area 737	Area 738	Area 739	Area 740	Area 741	Area 742	Area 743	Area 744	Area 745	Area 746	Area 747	Area 748	Area 749	Area 750	Area 751	Area 752	Area 753	Area 754	Area 755	Area 756	Area 757	Area 758	Area 759	Area 760	Area 761	Area 762	Area 763	Area 764	Area 765	Area 766	Area 767	Area 768	Area 769	Area 770	Area 771	Area 772	Area 773	Area 774	Area 775	Area 776	Area 777	Area 778	Area 779	Area 780	Area 781	Area 782	Area 783	Area 784	Area 785	Area 786	Area 787	Area 788	Area 789	Area 790	Area 791	Area 792	Area 793	Area 794	Area 795	Area 796	Area 797	Area 798	Area 799	Area 800	Area 801	Area 802	Area 803	Area 804	Area 805	Area 806	Area 807	Area 808	Area 809	Area 810	Area 811	Area 812	Area 813	Area 814	Area 815	Area 816	Area 817	Area 818	Area 819	Area 820	Area 821	Area 822	Area 823	Area 824	Area 825	Area 826	Area 827	Area 828	Area 829	Area 830	Area 831	Area 832	Area 833	Area 834	Area 835	Area 836	Area 837	Area 838	Area 839	Area 840	Area 841	Area 842	Area 843	Area 844	Area 845	Area 846	Area 847	Area 848	Area 849	Area 850	Area 851	Area 852	Area 853	Area 854	Area 855	Area 856	Area 857	Area 858	Area 859	Area 860	Area 861	Area 862	Area 863	Area 864	Area 865	Area 866	Area 867	Area 868	Area 869	Area 870	Area 871	Area 872	Area 873	Area 874	Area 875	Area 876	Area 877	Area 878	Area 879	Area 880	Area 881	Area 882	Area 883	Area 884	Area 885	Area 886	Area 887	Area 888	Area 889	Area 890	Area 891	Area 892	Area 893	Area 894	Area 895	Area 896	Area 897	Area 898	Area 899	Area 900	Area 901	Area 902	Area 903	Area 904	Area 905	Area 906	Area 907	Area 908	Area 909	Area 910	Area 911	Area 912	Area 913	Area 914	Area 915	Area 916	Area 917	Area 918	Area 919	Area 920	Area 921	Area 922	Area 923	Area 924	Area 925	Area 926	Area 927	Area 928	Area 929	Area 930	Area 931	Area 932	Area 933	Area 934	Area 935	Area 936	Area 937	Area 938	Area 939	Area 940	Area 941	Area 942	Area 943	Area 944	Area 945	Area 946	Area 947	Area 948	Area 949	Area 950	Area 951	Area 952	Area 953	Area 954	Area 955	Area 956	Area 957	Area 958	Area 959	Area 960	Area 961	Area 962	Area 963	Area 964	Area 965	Area 966	Area 967	Area 968	Area 969	Area 970	Area 971	Area 972	Area 973	Area 974	Area 975	Area 976	Area 977	Area 978	Area 979	Area 980	Area 981	Area 982	Area 983	Area 984	Area 985	Area 986	Area 987	Area 988	Area 989	Area 990	Area 991	Area 992	Area 993	Area 994	Area 995	Area 996	Area 997	Area 998	Area 999	Area 1000
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CCGNAME	1971-7814	AB Virus (no heteroduplex)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PROTEIN	1971-7814	VIRUS	13-40	111-145							AREA9
MINOR OUTER CAPSID PROTEIN	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN RV-5)	13-40	111-145							
MINOR OUTER CAPSID PROTEIN	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 2 / STRAIN DS1)	13-40	111-145							
MINOR OUTER CAPSID PROTEIN	MINOR OUTER CAPSID PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 1 / STRAIN WA)	111-145								
MINOR OUTER CAPSID PROTEIN	MINOR OUTER CAPSID PROTEIN	RABBIT ROTAVIRUS (STRAIN ALABAMA)	111-145								
MINOR OUTER CAPSID PROTEIN	MINOR OUTER CAPSID PROTEIN	SIMIAN 11 ROTAVIRUS (STRAIN SA11)	111-146								
SMALL HYDROPHOBIC PROTEIN	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS	9-46								
SMALL HYDROPHOBIC PROTEIN	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN MATSUYAMA)	12-41								
SMALL HYDROPHOBIC PROTEIN	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN BELFAST)	9-41								
SMALL HYDROPHOBIC PROTEIN	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN ENDERS)	9-46								
SMALL HYDROPHOBIC PROTEIN	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN LEVY-LYNH)	9-46								
SMALL HYDROPHOBIC PROTEIN	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN KILIJAM)	9-46								
SMALL HYDROPHOBIC PROTEIN	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN BRISTOL 1)	9-46								
SMALL HYDROPHOBIC PROTEIN	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN MUYAHARA VACCINE)	12-41								
SMALL HYDROPHOBIC PROTEIN	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN RV)	9-41								
SMALL HYDROPHOBIC PROTEIN	SMALL HYDROPHOBIC PROTEIN	MUMPS VIRUS (STRAIN URABE VACCINE AM9)	12-41								
SIGMA 1 PROTEIN PRECURSOR	SIGMA 1 PROTEIN PRECURSOR	NEOVIRUS (TYPE 2 / STRAIN DEARING)	26-53	21-122	127-168	222-259					
SIGMA 1 PROTEIN PRECURSOR	SIGMA 1 PROTEIN PRECURSOR	NEOVIRUS (TYPE 2 / STRAIN DSWOMES)	4-104	110-193							
SIGMA 2 PROTEIN	SIGMA 2 PROTEIN	NEOVIRUS (TYPE 1 / STRAIN LANG)	4-53	35-104	112-160						
SIGMA 3 PROTEIN	SIGMA 3 PROTEIN	NEOVIRUS (TYPE 2 / STRAIN DEARING)	310-314								
SIGMA 1-3 PROTEIN	SIGMA 1-3 PROTEIN	NEOVIRUS (TYPE 2 / STRAIN DSWOMES)	289-316								
SIGMA 1-3 PROTEIN	SIGMA 1-3 PROTEIN	NEOVIRUS (TYPE 2 / STRAIN DEARING)	90-117								
SIGMA 1-3 PROTEIN	SIGMA 1-3 PROTEIN	NEOVIRUS (TYPE 1 / STRAIN LANG)	50-77								
PROTEIN T1A	PROTEIN T1A	CAPRIPOXVIRUS (STRAIN INS-1)	124-134								
PROTEIN T1	PROTEIN T1	SHOPE FIBROMA VIRUS (STRAIN KASZA)	210-217								
PROBABLE DNA PACKAGING PROTEIN	PROBABLE DNA PACKAGING PROTEIN	EPSTEIN-BARR VIRUS (STRAIN B95-4)	214-290								
PROBABLE DNA PACKAGING PROTEIN	PROBABLE DNA PACKAGING PROTEIN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	417-421								
PROBABLE DNA PACKAGING PROTEIN	PROBABLE DNA PACKAGING PROTEIN	HUMAN CYTOMEGALOVIRUS (TYPE 6 / STRAIN UK-AMN-1102)	176-281								
PROBABLE DNA PACKAGING PROTEIN	PROBABLE DNA PACKAGING PROTEIN	ICTALURID HERPESVIRUS 1	710-737								
PROBABLE DNA PACKAGING PROTEIN	PROBABLE DNA PACKAGING PROTEIN	VACCINELLA-ZOSTER VIRUS (STRAIN DUMAS)	394-421								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	THELAPHORPTEUS TENAX VIRUS 1 (STRAIN V73)	169-186								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	THELAPHORPTEUS TENAX VIRUS 1 (STRAIN KRA1)	169-186								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	HUMAN PARAINFLUENZA A VIRUS (STRAIN TOSHIBA)	4-38								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	23-65								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	4-61								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	30-78								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	33-87								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	TORACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)	33-112								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	AUTOGRAHA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	39-86								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	5-39								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	80-107								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	AUTOGRAHA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	72-111								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	9-36	110-131							
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	34-61								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	MAIZE STREAK VIRUS (NIGERIAN ISOLATE)	34-61								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	MAIZE STREAK VIRUS (SOUTH-AFRICAN ISOLATE)	34-61								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	76-103								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	93-164								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	118-148								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SOYBEAN CHLOROTIC MOTTLE VIRUS	24-87								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	231-267								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	133-184								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	AUTOGRAHA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS	122-149								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SOYBEAN CHLOROTIC MOTTLE VIRUS	56-94								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SOYBEAN CHLOROTIC MOTTLE VIRUS	81-121	546-573	651-700						
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SULFOLOBUS VIRUS-LIKE PARTICLE SSV1	13-40								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	SOYBEAN CHLOROTIC MOTTLE VIRUS	74-108	152-179	184-218						
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
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VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89								
VIRAL PROTEIN TPX	VIRAL PROTEIN TPX	FOWLPOX VIRUS (ISOLATE HP-43H[MUNICH])	62-89						</		

[illegible]

TABLE VII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

(PREFERRED VIRAL SEQUENCES)

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PCGENE	PROTEIN	PROTEIN (see Description)	ORF1	ORF2	ORF3	ORF4	ORF5	ORF6	ORF7	ORF8	ORF9	ORF10	ORF11	ORF12	ORF13	ORF14	ORF15	ORF16	ORF17	ORF18	ORF19	ORF20	ORF21	ORF22	ORF23	ORF24	ORF25	ORF26	ORF27	ORF28	ORF29	ORF30	ORF31	ORF32	ORF33	ORF34	ORF35	ORF36	ORF37	ORF38	ORF39	ORF40	ORF41	ORF42	ORF43	ORF44	ORF45	ORF46	ORF47	ORF48	ORF49	ORF50	ORF51	ORF52	ORF53	ORF54	ORF55	ORF56	ORF57	ORF58	ORF59	ORF60	ORF61	ORF62	ORF63	ORF64	ORF65	ORF66	ORF67	ORF68	ORF69	ORF70	ORF71	ORF72	ORF73	ORF74	ORF75	ORF76	ORF77	ORF78	ORF79	ORF80	ORF81	ORF82	ORF83	ORF84	ORF85	ORF86	ORF87	ORF88	ORF89	ORF90	ORF91	ORF92	ORF93	ORF94	ORF95	ORF96	ORF97	ORF98	ORF99	ORF100	ORF101	ORF102	ORF103	ORF104	ORF105	ORF106	ORF107	ORF108	ORF109	ORF110	ORF111	ORF112	ORF113	ORF114	ORF115	ORF116	ORF117	ORF118	ORF119	ORF120	ORF121	ORF122	ORF123	ORF124	ORF125	ORF126	ORF127	ORF128	ORF129	ORF130	ORF131	ORF132	ORF133	ORF134	ORF135	ORF136	ORF137	ORF138	ORF139	ORF140	ORF141	ORF142	ORF143	ORF144	ORF145	ORF146	ORF147	ORF148	ORF149	ORF150	ORF151	ORF152	ORF153	ORF154	ORF155	ORF156	ORF157	ORF158	ORF159	ORF160	ORF161	ORF162	ORF163	ORF164	ORF165	ORF166	ORF167	ORF168	ORF169	ORF170	ORF171	ORF172	ORF173	ORF174	ORF175	ORF176	ORF177	ORF178	ORF179	ORF180	ORF181	ORF182	ORF183	ORF184	ORF185	ORF186	ORF187	ORF188	ORF189	ORF190	ORF191	ORF192	ORF193	ORF194	ORF195	ORF196	ORF197	ORF198	ORF199	ORF200	ORF201	ORF202	ORF203	ORF204	ORF205	ORF206	ORF207	ORF208	ORF209	ORF210	ORF211	ORF212	ORF213	ORF214	ORF215	ORF216	ORF217	ORF218	ORF219	ORF220	ORF221	ORF222	ORF223	ORF224	ORF225	ORF226	ORF227	ORF228	ORF229	ORF230	ORF231	ORF232	ORF233	ORF234	ORF235	ORF236	ORF237	ORF238	ORF239	ORF240	ORF241	ORF242	ORF243	ORF244	ORF245	ORF246	ORF247	ORF248	ORF249	ORF250	ORF251	ORF252	ORF253	ORF254	ORF255	ORF256	ORF257	ORF258	ORF259	ORF260	ORF261	ORF262	ORF263	ORF264	ORF265	ORF266	ORF267	ORF268	ORF269	ORF270	ORF271	ORF272	ORF273	ORF274	ORF275	ORF276	ORF277	ORF278	ORF279	ORF280	ORF281	ORF282	ORF283	ORF284	ORF285	ORF286	ORF287	ORF288	ORF289	ORF290	ORF291	ORF292	ORF293	ORF294	ORF295	ORF296	ORF297	ORF298	ORF299	ORF300	ORF301	ORF302	ORF303	ORF304	ORF305	ORF306	ORF307	ORF308	ORF309	ORF310	ORF311	ORF312	ORF313	ORF314	ORF315	ORF316	ORF317	ORF318	ORF319	ORF320	ORF321	ORF322	ORF323	ORF324	ORF325	ORF326	ORF327	ORF328	ORF329	ORF330	ORF331	ORF332	ORF333	ORF334	ORF335	ORF336	ORF337	ORF338	ORF339	ORF340	ORF341	ORF342	ORF343	ORF344	ORF345	ORF346	ORF347	ORF348	ORF349	ORF350	ORF351	ORF352	ORF353	ORF354	ORF355	ORF356	ORF357	ORF358	ORF359	ORF360	ORF361	ORF362	ORF363	ORF364	ORF365	ORF366	ORF367	ORF368	ORF369	ORF370	ORF371	ORF372	ORF373	ORF374	ORF375	ORF376	ORF377	ORF378	ORF379	ORF380	ORF381	ORF382	ORF383	ORF384	ORF385	ORF386	ORF387	ORF388	ORF389	ORF390	ORF391	ORF392	ORF393	ORF394	ORF395	ORF396	ORF397	ORF398	ORF399	ORF400	ORF401	ORF402	ORF403	ORF404	ORF405	ORF406	ORF407	ORF408	ORF409	ORF410	ORF411	ORF412	ORF413	ORF414	ORF415	ORF416	ORF417	ORF418	ORF419	ORF420	ORF421	ORF422	ORF423	ORF424	ORF425	ORF426	ORF427	ORF428	ORF429	ORF430	ORF431	ORF432	ORF433	ORF434	ORF435	ORF436	ORF437	ORF438	ORF439	ORF440	ORF441	ORF442	ORF443	ORF444	ORF445	ORF446	ORF447	ORF448	ORF449	ORF450	ORF451	ORF452	ORF453	ORF454	ORF455	ORF456	ORF457	ORF458	ORF459	ORF460	ORF461	ORF462	ORF463	ORF464	ORF465	ORF466	ORF467	ORF468	ORF469	ORF470	ORF471	ORF472	ORF473	ORF474	ORF475	ORF476	ORF477	ORF478	ORF479	ORF480	ORF481	ORF482	ORF483	ORF484	ORF485	ORF486	ORF487	ORF488	ORF489	ORF490	ORF491	ORF492	ORF493	ORF494	ORF495	ORF496	ORF497	ORF498	ORF499	ORF500	ORF501	ORF502	ORF503	ORF504	ORF505	ORF506	ORF507	ORF508	ORF509	ORF510	ORF511	ORF512	ORF513	ORF514	ORF515	ORF516	ORF517	ORF518	ORF519	ORF520	ORF521	ORF522	ORF523	ORF524	ORF525	ORF526	ORF527	ORF528	ORF529	ORF530	ORF531	ORF532	ORF533	ORF534	ORF535	ORF536	ORF537	ORF538	ORF539	ORF540	ORF541	ORF542	ORF543	ORF544	ORF545	ORF546	ORF547	ORF548	ORF549	ORF550	ORF551	ORF552	ORF553	ORF554	ORF555	ORF556	ORF557	ORF558	ORF559	ORF560	ORF561	ORF562	ORF563	ORF564	ORF565	ORF566	ORF567	ORF568	ORF569	ORF570	ORF571	ORF572	ORF573	ORF574	ORF575	ORF576	ORF577	ORF578	ORF579	ORF580	ORF581	ORF582	ORF583	ORF584	ORF585	ORF586	ORF587	ORF588	ORF589	ORF590	ORF591	ORF592	ORF593	ORF594	ORF595	ORF596	ORF597	ORF598	ORF599	ORF600	ORF601	ORF602	ORF603	ORF604	ORF605	ORF606	ORF607	ORF608	ORF609	ORF610	ORF611	ORF612	ORF613	ORF614	ORF615	ORF616	ORF617	ORF618	ORF619	ORF620	ORF621	ORF622	ORF623	ORF624	ORF625	ORF626	ORF627	ORF628	ORF629	ORF630	ORF631	ORF632	ORF633	ORF634	ORF635	ORF636	ORF637	ORF638	ORF639	ORF640	ORF641	ORF642	ORF643	ORF644	ORF645	ORF646	ORF647	ORF648	ORF649	ORF650	ORF651	ORF652	ORF653	ORF654	ORF655	ORF656	ORF657	ORF658	ORF659	ORF660	ORF661	ORF662	ORF663	ORF664	ORF665	ORF666	ORF667	ORF668	ORF669	ORF670	ORF671	ORF672	ORF673	ORF674	ORF675	ORF676	ORF677	ORF678	ORF679	ORF680	ORF681	ORF682	ORF683	ORF684	ORF685	ORF686	ORF687	ORF688	ORF689	ORF690	ORF691	ORF692	ORF693	ORF694	ORF695	ORF696	ORF697	ORF698	ORF699	ORF700	ORF701	ORF702	ORF703	ORF704	ORF705	ORF706	ORF707	ORF708	ORF709	ORF710	ORF711	ORF712	ORF713	ORF714	ORF715	ORF716	ORF717	ORF718	ORF719	ORF720	ORF721	ORF722	ORF723	ORF724	ORF725	ORF726	ORF727	ORF728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GENE	1971-1974	ALL VIRUSES (see Distribution Table)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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TABLE VIII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL PROCARYOTIC PROTEINS

[illegible]

PCGENE	1011164	Protein/peptide Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
PROTEIN	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393</																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															

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PCGENE	1974/1984	Proteinase Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PRGAL	PROTEIN	ORGANISM	124-851								
PRGAL	BETA-GALACTOSIDASE	CLOSTRIDIUM ACETOBYTILICUM	161-191								
PRGAL	BETA-GALACTOSIDASE	CLOSTRIDIUM THERMOSULFURIGENIS	245-272								
PRGAL	BETA-GALACTOSIDASE	KLEBSIELLA PNEUMONIAE	305-332								
PRGAL	BETA-GALACTOSIDASE	LACTOBACILLUS DELBRUECKII	188-215								
PRGAL	BETA-GALACTOSIDASE	STREPTOCOCCUS THERMOPHILUS	179-206								
PRGAL	BETA-GALACTOSIDASE	SULFOLOBUS SOLFATARICUS	139-156								
PRGAL	BETA-GALACTOSIDASE	LEUCOSTOCCUS LACTIS	108-140								
PRGAL	BETA-GALACTOSIDASE	SULFOLOBUS SOLFATARICUS	333-380	411-443							
PRGAL	BETA-GALACTOSIDASE	CLOSTRIDIUM THERMOCELLUM	239-286	371-409	611-665						
PRGAL	BETA-GALACTOSIDASE	CLOSTRIDIUM THERMOCELLUM	484-494	536-563							
PRGAL	BETA-GALACTOSIDASE	ESCHERICHIA COLI	421-448								
PRGAL	BETA-GALACTOSIDASE	AGROBACTERIUM SP	85-112	413-462	692-719	718-765					
PRGAL	BETA-GALACTOSIDASE	BUTYRIBACTERIUM FIBRISOLVENS	60-87								
PRGAL	BETA-GALACTOSIDASE	STAPHYLOCOCCUS AUREUS	161-197								
PRGAL	BETA-GALACTOSIDASE	STAPHYLOCOCCUS AUREUS	163-190								
PRGAL	BETA-GALACTOSIDASE	STAPHYLOCOCCUS AUREUS	33-60								
PRGAL	BETA-GALACTOSIDASE	BACILLUS SPIRILLICUS	145-172								
PRGAL	BETA-GALACTOSIDASE	BACILLUS SPIRILLICUS	136-157								
PRGAL	BETA-GALACTOSIDASE	ESCHERICHIA COLI	144-171								
PRGAL	BETA-GALACTOSIDASE	BACILLUS SPIRILLICUS	91-118	215-305							
PRGAL	BETA-GALACTOSIDASE	BACILLUS CEREUS	152-179	204-231							
PRGAL	BETA-GALACTOSIDASE	HAEMOPHILUS INFLUENZAE	18-47	201-228							
PRGAL	BETA-GALACTOSIDASE	BACILLUS CEREUS	18-47								
PRGAL	BETA-GALACTOSIDASE	BACILLUS SP	15-33	91-129							
PRGAL	BETA-GALACTOSIDASE	BACILLUS CEREUS	15-30								
PRGAL	BETA-GALACTOSIDASE	PSEUDOMONAS AERUGINOSA	30-48	200-227							
PRGAL	BETA-GALACTOSIDASE	BACILLUS CEREUS	22-49								
PRGAL	BETA-GALACTOSIDASE	BACTEROIDES FRAGILIS	91-120	276-303							
PRGAL	BETA-GALACTOSIDASE	BACILLUS CEREUS	47-74	86-113							
PRGAL	BETA-GALACTOSIDASE	BACILLUS LICHENIFORMIS	191-221								
PRGAL	BETA-GALACTOSIDASE	PROTEUS MORGANII	4-38	240-267							
PRGAL	BETA-GALACTOSIDASE	PROTEUS VULGARIS	41-70								
PRGAL	BETA-GALACTOSIDASE	STREPTOMYCES ALBUS G	121-148								
PRGAL	BETA-GALACTOSIDASE	KLEBSIELLA PNEUMONIAE	19-74	99-126							
PRGAL	BETA-GALACTOSIDASE	STAPHYLOCOCCUS AUREUS	118-144	233-263							
PRGAL	BETA-GALACTOSIDASE	ESCHERICHIA COLI	135-199								
PRGAL	BETA-GALACTOSIDASE	ESCHERICHIA COLI	129-156	315-332							
PRGAL	BETA-GALACTOSIDASE	BACILLUS LICHENIFORMIS	87-114	122-161	274-281	303-339					
PRGAL	BETA-GALACTOSIDASE	STAPHYLOCOCCUS AUREUS	312-346								
PRGAL	BETA-GALACTOSIDASE	TRYPANOSA PALLIDUM	372-394								
PRGAL	BETA-GALACTOSIDASE	BACILLUS SUBTILIS	16-63								
PRGAL	BETA-GALACTOSIDASE	PSEUDOMONAS PUTIDA	119-133								
PRGAL	BETA-GALACTOSIDASE	PSEUDOMONAS PUTIDA	179-213								
PRGAL	BETA-GALACTOSIDASE	DESULFURELLOBUS AMBIVALENS	260-287	242-290	311-355	391-435	540-573				
PRGAL	BETA-GALACTOSIDASE	PSEUDOMONAS AERUGINOSA	334-381	312-340							
PRGAL	BETA-GALACTOSIDASE	PSEUDOMONAS AERUGINOSA	7-34								
PRGAL	BETA-GALACTOSIDASE	PSEUDOMONAS AERUGINOSA	419-466								
PRGAL	BETA-GALACTOSIDASE	ESCHERICHIA COLI	6-33								
PRGAL	BETA-GALACTOSIDASE	ESCHERICHIA COLI	174-203								
PRGAL	BETA-GALACTOSIDASE	BORDETELLA PERTUSSIS	116-143								
PRGAL	BETA-GALACTOSIDASE	BORDETELLA PERTUSSIS	39-66	202-229							
PRGAL	BETA-GALACTOSIDASE	BORDETELLA PERTUSSIS	113-143	341-368							
PRGAL	BETA-GALACTOSIDASE	BORDETELLA PERTUSSIS	313-340	686-719							
PRGAL	BETA-GALACTOSIDASE	CLOSTRIDIUM BOTULINUM	646-693	726-763	802-833	851-890	968-995	1004-1031	1018-1089	1119-1207	
PRGAL	BETA-GALACTOSIDASE	CLOSTRIDIUM BOTULINUM									

GENE	PROTEIN	FUNCTION	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
BTX1	PROTEIN	BTX1	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX2	PROTEIN	BTX2	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX3	PROTEIN	BTX3	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX4	PROTEIN	BTX4	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX5	PROTEIN	BTX5	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX6	PROTEIN	BTX6	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX7	PROTEIN	BTX7	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX8	PROTEIN	BTX8	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX9	PROTEIN	BTX9	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX10	PROTEIN	BTX10	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX11	PROTEIN	BTX11	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX12	PROTEIN	BTX12	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX13	PROTEIN	BTX13	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX14	PROTEIN	BTX14	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX15	PROTEIN	BTX15	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX16	PROTEIN	BTX16	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX17	PROTEIN	BTX17	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX18	PROTEIN	BTX18	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX19	PROTEIN	BTX19	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX20	PROTEIN	BTX20	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX21	PROTEIN	BTX21	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX22	PROTEIN	BTX22	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX23	PROTEIN	BTX23	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX24	PROTEIN	BTX24	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX25	PROTEIN	BTX25	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX26	PROTEIN	BTX26	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX27	PROTEIN	BTX27	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX28	PROTEIN	BTX28	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX29	PROTEIN	BTX29	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX30	PROTEIN	BTX30	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX31	PROTEIN	BTX31	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX32	PROTEIN	BTX32	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX33	PROTEIN	BTX33	CLOSTRIDIUM BOTULINUM	84-113	314-341	710-770	798-825	850-892				
BTX34	PROTEIN	BTX34	CLOSTRIDIUM BOTULINUM</									

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[illegible]

PCPNAME	10111144	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PCP1	PCP1	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7
PCP2	PCP2	BACILLUS THURINGIENSIS	100-226	101-218	102-210	103-202	104-194	105-186	106-178
PCP3	PCP3	BACILLUS THURINGIENSIS	107-233	108-225	109-217	110-209	111-201	112-193	113-185
PCP4	PCP4	BACILLUS THURINGIENSIS	114-240	115-232	116-224	117-216	118-208	119-200	120-192
PCP5	PCP5	BACILLUS THURINGIENSIS	121-247	122-239	123-231	124-223	125-215	126-207	127-199
PCP6	PCP6	BACILLUS THURINGIENSIS	128-254	129-246	130-238	131-230	132-222	133-214	134-206
PCP7	PCP7	BACILLUS THURINGIENSIS	135-261	136-253	137-245	138-237	139-229	140-221	141-213
PCP8	PCP8	BACILLUS THURINGIENSIS	142-268	143-260	144-252	145-244	146-236	147-228	148-220
PCP9	PCP9	BACILLUS THURINGIENSIS	149-275	150-267	151-259	152-251	153-243	154-235	155-227
PCP10	PCP10	BACILLUS THURINGIENSIS	156-282	157-274	158-266	159-258	160-250	161-242	162-234
PCP11	PCP11	BACILLUS THURINGIENSIS	163-289	164-281	165-273	166-265	167-257	168-249	169-241
PCP12	PCP12	BACILLUS THURINGIENSIS	170-296	171-288	172-280	173-272	174-264	175-256	176-248
PCP13	PCP13	BACILLUS THURINGIENSIS	177-303	178-295	179-287	180-279	181-271	182-263	183-255
PCP14	PCP14	BACILLUS THURINGIENSIS	184-310	185-302	186-294	187-286	188-278	189-270	190-262
PCP15	PCP15	BACILLUS THURINGIENSIS	191-317	192-309	193-301	194-293	195-285	196-277	197-269
PCP16	PCP16	BACILLUS THURINGIENSIS	198-324	199-316	200-308	201-300	202-292	203-284	204-276
PCP17	PCP17	BACILLUS THURINGIENSIS	205-331	206-323	207-315	208-307	209-299	210-291	211-283
PCP18	PCP18	BACILLUS THURINGIENSIS	212-338	213-330	214-322	215-314	216-306	217-298	218-290
PCP19	PCP19	BACILLUS THURINGIENSIS	219-345	220-337	221-329	222-321	223-313	224-305	225-297
PCP20	PCP20	BACILLUS THURINGIENSIS	226-352	227-344	228-336	229-328	230-320	231-312	232-304
PCP21	PCP21	BACILLUS THURINGIENSIS	233-359	234-351	235-343	236-335	237-327	238-319	239-311
PCP22	PCP22	BACILLUS THURINGIENSIS	240-366	241-358	242-350	243-342	244-334	245-326	246-318
PCP23	PCP23	BACILLUS THURINGIENSIS	247-373	248-365	249-357	250-349	251-341	252-333	253-325
PCP24	PCP24	BACILLUS THURINGIENSIS	254-380	255-372	256-364	257-356	258-348	259-340	260-332
PCP25	PCP25	BACILLUS THURINGIENSIS	261-387	262-379	263-371	264-363	265-355	266-347	267-339
PCP26	PCP26	BACILLUS THURINGIENSIS	268-394	269-386	270-378	271-370	272-362	273-354	274-346
PCP27	PCP27	BACILLUS THURINGIENSIS	275-401	276-393	277-385	278-377	279-369	280-361	281-353
PCP28	PCP28	BACILLUS THURINGIENSIS	282-408	283-400	284-392	285-384	286-376	287-368	288-360
PCP29	PCP29	BACILLUS THURINGIENSIS	289-415	290-407	291-399	292-391	293-383	294-375	295-367
PCP30	PCP30	BACILLUS THURINGIENSIS	296-422	297-414	298-406	299-398	300-390	301-382	302-374
PCP31	PCP31	BACILLUS THURINGIENSIS	303-429	304-421	305-413	306-405	307-397	308-389	309-381
PCP32	PCP32	BACILLUS THURINGIENSIS	310-436	311-428	312-420	313-412	314-404	315-396	316-388
PCP33	PCP33	BACILLUS THURINGIENSIS	317-443	318-435	319-427	320-419	321-411	322-403	323-395
PCP34	PCP34	BACILLUS THURINGIENSIS	324-450	325-442	326-434	327-426	328-418	329-410	330-402
PCP35	PCP35	BACILLUS THURINGIENSIS	331-457	332-449	333-441	334-433	335-425	336-417	337-409
PCP36	PCP36	BACILLUS THURINGIENSIS	338-464	339-456	340-448	341-440	342-432	343-424	344-416
PCP37	PCP37	BACILLUS THURINGIENSIS	345-471	346-463	347-455	348-447	349-439	350-431	351-423
PCP38	PCP38	BACILLUS THURINGIENSIS	352-478	353-470	354-462	355-454	356-446	357-438	358-430
PCP39	PCP39	BACILLUS THURINGIENSIS	359-485	360-477	361-469	362-461	363-453	364-445	365-437
PCP40	PCP40	BACILLUS THURINGIENSIS	366-492	367-484	368-476	369-468	370-460	371-452	372-444
PCP41	PCP41	BACILLUS THURINGIENSIS	373-499	374-491	375-483	376-475	377-467	378-459	379-451
PCP42	PCP42	BACILLUS THURINGIENSIS	380-506	381-498	382-490	383-482	384-474	385-466	386-458
PCP43	PCP43	BACILLUS THURINGIENSIS	387-513	388-505	389-497	390-489	391-481	392-473	393-465
PCP44	PCP44	BACILLUS THURINGIENSIS	394-520	395-512	396-504	397-496	398-488	399-480	400-472
PCP45	PCP45	BACILLUS THURINGIENSIS	401-527	402-519	403-511	404-503	405-495	406-487	407-479
PCP46	PCP46	BACILLUS THURINGIENSIS	408-534	409-526	410-518	411-510	412-502	413-494	414-486
PCP47	PCP47	BACILLUS THURINGIENSIS	415-541	416-533	417-525	418-517	419-509	420-501	421-493
PCP48	PCP48	BACILLUS THURINGIENSIS	422-548	423-540	424-532	425-524	426-516	427-508	428-500
PCP49	PCP49	BACILLUS THURINGIENSIS	429-555	430-547	431-539	432-531	433-523	434-515	435-507
PCP50	PCP50	BACILLUS THURINGIENSIS	436-562	437-554	438-546	439-538	440-530	441-522	442-514
PCP51	PCP51	BACILLUS THURINGIENSIS	443-569	444-561	445-553	446-545	447-537	448-529	449-521
PCP52	PCP52	BACILLUS THURINGIENSIS	450-576	451-568	452-560	453-552	454-544	455-536	456-528
PCP53	PCP53	BACILLUS THURINGIENSIS	457-583	458-575	459-567	460-559	461-551	462-543	463-535
PCP54	PCP54	BACILLUS THURINGIENSIS	464-590	465-582	466-574	467-566	468-558	469-550	470-542
PCP55	PCP55	BACILLUS THURINGIENSIS	471-597	472-589	473-581	474-573	475-565	476-557	477-549
PCP56	PCP56	BACILLUS THURINGIENSIS	478-604	479-596	480-588	481-580	482-572	483-564	484-556
PCP57	PCP57	BACILLUS THURINGIENSIS	485-611	486-603	487-595	488-587	489-579	490-571	491-563
PCP58	PCP58	BACILLUS THURINGIENSIS	492-618	493-610	494-602	495-594	496-586	497-578	498-570
PCP59	PCP59	BACILLUS THURINGIENSIS	499-625	500-617	501-609	502-601	503-593	504-585	505-577
PCP60	PCP60	BACILLUS THURINGIENSIS	506-632	507-624	508-616	509-608	510-600	511-592	512-584
PCP61	PCP61	BACILLUS THURINGIENSIS	513-639	514-631	515-623	516-615	517-607	518-599	519-591
PCP62	PCP62	BACILLUS THURINGIENSIS	520-646	521-638	522-630	523-622	524-614	525-606	526-598
PCP63	PCP63	BACILLUS THURINGIENSIS	527-653	528-645	529-637	530-629	531-621	532-613	533-605
PCP64	PCP64	BACILLUS THURINGIENSIS	534-660	535-652	536-644	537-636	538-628	539-620	540-612
PCP65	PCP65	BACILLUS THURINGIENSIS	541-667	542-659	543-651	544-643	545-635	546-627	547-619
PCP66	PCP66	BACILLUS THURINGIENSIS	548-674	549-666	550-658	551-650	552-642	553-634	554-626
PCP67	PCP67	BACILLUS THURINGIENSIS	555-681	556-673	557-665	558-657	559-649	560-641	561-633
PCP68	PCP68	BACILLUS THURINGIENSIS	562-688	563-680	564-672	565-664	566-656	567-648	568-640
PCP69	PCP69	BACILLUS THURINGIENSIS	569-695	570-687	571-679	572-671	573-663	574-655	575-647
PCP70	PCP70	BACILLUS THURINGIENSIS	576-702	577-694	578-686	579-678	580-670	581-662	582-654
PCP71	PCP71	BACILLUS THURINGIENSIS	583-709	584-701	585-693	586-685	587-677	588-669	589-661
PCP72	PCP72	BACILLUS THURINGIENSIS	590-716	591-708	592-700	593-692	594-684	595-676	596-668
PCP73	PCP73	BACILLUS THURINGIENSIS	597-723	598-715	599-707	600-699	601-691	602-683	603-675
PCP74	PCP74	BACILLUS THURINGIENSIS	604-730	605-722	606-714	607-706	608-698	609-690	610-682
PCP75	PCP75	BACILLUS THURINGIENSIS	611-737	612-729	613-721	614-713	615-705	616-697	617-689
PCP76	PCP76	BACILLUS THURINGIENSIS	618-744	619-736	620-728	621-720	622-712	623-704	624-696
PCP77	PCP77	BACILLUS THURINGIENSIS	625-751	626-743	627-735	628-727	629-719	630-711	631-703
PCP78	PCP78	BACILLUS THURINGIENSIS	632-758	633-750	634-742	635-734	636-726	637-718	638-710
PCP79	PCP79	BACILLUS THURINGIENSIS	639-765	640-757	641-749	642-741	643-733	644-725	645-717
PCP80	PCP80	BACILLUS THURINGIENSIS	646-772	647-764	648-756	649-748	650-740	651-732	652-724
PCP81	PCP81	BACILLUS THURINGIENSIS	653-779	654-771	655-763	656-755	657-747	658-739	659-731
PCP82	PCP82	BACILLUS THURINGIENSIS	660-786	661-778	662-770	663-762	664-754	665-746	666-738
PCP83	PCP83	BACILLUS THURINGIENSIS	667-793	668-785	669-777	670-769	671-761	672-753	673-745
PCP84	PCP84	BACILLUS THURINGIENSIS	674-800	675-792	676-784	677-776	678-768	679-760	680-752
PCP85	PCP85	BACILLUS THURINGIENSIS	681-807	682-799	683-791	684-783	685-775	686-767	687-759
PCP86	PCP86	BACILLUS THURINGIENSIS	688-814	689-806	690-798	691-790	692-782	693-774	694-766
PCP87	PCP87	BACILLUS THURINGIENSIS	695-821	696-813	697-805	698-797	699-789	700-781	701-773
PCP88	PCP88	BACILLUS THURINGIENSIS	702-828	703-820	704-812	705-804	706-796	707-788	708-780
PCP89	PCP89	BACILLUS THURINGIENSIS	709-835	710-827	711-819	712-811	713-803	714-795	715-787
PCP90	PCP90	BACILLUS THURINGIENSIS	716-842	717-834	718-826	719-818	720-810	721-802	722-794
PCP91	PCP91	BACILLUS THURINGIENSIS	723-849	724-841	725-833	726-825	727-817	728-809	729-801
PCP92	PCP92	BACILLUS THURINGIENSIS	730-856	731-848	732-840	733-832	734-824	735-816	736-808
PCP93	PCP93	BACILLUS THURINGIENSIS	737-863	738-855	739-847	740-839	741-831	742-823	743-815
PCP94	PCP94	BACILLUS THURINGIENSIS	744-870	745-862	746-854	747-846	748-838	749-830	750-822
PCP95	PCP95	BACILLUS THURINGIENSIS	751-877	752-869	753-861	754-853	755-845	756-837	757-829
PCP96	PCP96	BACILLUS THURINGIENSIS	758-884	759-876	760-868	761-860	762-852	763-844	764-836
PCP97	PCP97	BACILLUS THURINGIENSIS	765-891	766-883	767-875	768-867	769-859	770-851	771-843
PCP98	PCP98	BACILLUS THURINGIENSIS	772-898	773-890	774-882	775-874	776-866	777-858	778-850
PCP99	PCP99	BACILLUS THURINGIENSIS	779-905	780-897	781-889	782-881	783-873	784-865	785-857
PCP100	PCP100	BACILLUS THURINGIENSIS	786-912	787-904	788-896	789-888	790-880	791-872	792-864
PCP101	PCP101	BACILLUS THURINGIENSIS	793-919	794-911	795-903	796-895	797-887	798-879	799-871
PCP102	PCP1								

PCGENE	1971-17144	Prokaryotic Sequences	ABR4.1	ABR4.2	ABR4.3	ABR4.4	ABR4.5	ABR4.6	ABR4.7	ABR4.8	ABR4.9	ABR4.10	ABR4.11	ABR4.12	ABR4.13	ABR4.14	ABR4.15	ABR4.16	ABR4.17	ABR4.18	ABR4.19	ABR4.20	ABR4.21	ABR4.22	ABR4.23	ABR4.24	ABR4.25	ABR4.26	ABR4.27	ABR4.28	ABR4.29	ABR4.30	ABR4.31	ABR4.32	ABR4.33	ABR4.34	ABR4.35	ABR4.36	ABR4.37	ABR4.38	ABR4.39	ABR4.40	ABR4.41	ABR4.42	ABR4.43	ABR4.44	ABR4.45	ABR4.46	ABR4.47	ABR4.48	ABR4.49	ABR4.50	ABR4.51	ABR4.52	ABR4.53	ABR4.54	ABR4.55	ABR4.56	ABR4.57	ABR4.58	ABR4.59	ABR4.60	ABR4.61	ABR4.62	ABR4.63	ABR4.64	ABR4.65	ABR4.66	ABR4.67	ABR4.68	ABR4.69	ABR4.70	ABR4.71	ABR4.72	ABR4.73	ABR4.74	ABR4.75	ABR4.76	ABR4.77	ABR4.78	ABR4.79	ABR4.80	ABR4.81	ABR4.82	ABR4.83	ABR4.84	ABR4.85	ABR4.86	ABR4.87	ABR4.88	ABR4.89	ABR4.90	ABR4.91	ABR4.92	ABR4.93	ABR4.94	ABR4.95	ABR4.96	ABR4.97	ABR4.98	ABR4.99	ABR4.100	ABR4.101	ABR4.102	ABR4.103	ABR4.104	ABR4.105	ABR4.106	ABR4.107	ABR4.108	ABR4.109	ABR4.110	ABR4.111	ABR4.112	ABR4.113	ABR4.114	ABR4.115	ABR4.116	ABR4.117	ABR4.118	ABR4.119	ABR4.120	ABR4.121	ABR4.122	ABR4.123	ABR4.124	ABR4.125	ABR4.126	ABR4.127	ABR4.128	ABR4.129	ABR4.130	ABR4.131	ABR4.132	ABR4.133	ABR4.134	ABR4.135	ABR4.136	ABR4.137	ABR4.138	ABR4.139	ABR4.140	ABR4.141	ABR4.142	ABR4.143	ABR4.144	ABR4.145	ABR4.146	ABR4.147	ABR4.148	ABR4.149	ABR4.150	ABR4.151	ABR4.152	ABR4.153	ABR4.154	ABR4.155	ABR4.156	ABR4.157	ABR4.158	ABR4.159	ABR4.160	ABR4.161	ABR4.162	ABR4.163	ABR4.164	ABR4.165	ABR4.166	ABR4.167	ABR4.168	ABR4.169	ABR4.170	ABR4.171	ABR4.172	ABR4.173	ABR4.174	ABR4.175	ABR4.176	ABR4.177	ABR4.178	ABR4.179	ABR4.180	ABR4.181	ABR4.182	ABR4.183	ABR4.184	ABR4.185	ABR4.186	ABR4.187	ABR4.188	ABR4.189	ABR4.190	ABR4.191	ABR4.192	ABR4.193	ABR4.194	ABR4.195	ABR4.196	ABR4.197	ABR4.198	ABR4.199	ABR4.200	ABR4.201	ABR4.202	ABR4.203	ABR4.204	ABR4.205	ABR4.206	ABR4.207	ABR4.208	ABR4.209	ABR4.210	ABR4.211	ABR4.212	ABR4.213	ABR4.214	ABR4.215	ABR4.216	ABR4.217	ABR4.218	ABR4.219	ABR4.220	ABR4.221	ABR4.222	ABR4.223	ABR4.224	ABR4.225	ABR4.226	ABR4.227	ABR4.228	ABR4.229	ABR4.230	ABR4.231	ABR4.232	ABR4.233	ABR4.234	ABR4.235	ABR4.236	ABR4.237	ABR4.238	ABR4.239	ABR4.240	ABR4.241	ABR4.242	ABR4.243	ABR4.244	ABR4.245	ABR4.246	ABR4.247	ABR4.248	ABR4.249	ABR4.250	ABR4.251	ABR4.252	ABR4.253	ABR4.254	ABR4.255	ABR4.256	ABR4.257	ABR4.258	ABR4.259	ABR4.260	ABR4.261	ABR4.262	ABR4.263	ABR4.264	ABR4.265	ABR4.266	ABR4.267	ABR4.268	ABR4.269	ABR4.270	ABR4.271	ABR4.272	ABR4.273	ABR4.274	ABR4.275	ABR4.276	ABR4.277	ABR4.278	ABR4.279	ABR4.280	ABR4.281	ABR4.282	ABR4.283	ABR4.284	ABR4.285	ABR4.286	ABR4.287	ABR4.288	ABR4.289	ABR4.290	ABR4.291	ABR4.292	ABR4.293	ABR4.294	ABR4.295	ABR4.296	ABR4.297	ABR4.298	ABR4.299	ABR4.300	ABR4.301	ABR4.302	ABR4.303	ABR4.304	ABR4.305	ABR4.306	ABR4.307	ABR4.308	ABR4.309	ABR4.310	ABR4.311	ABR4.312	ABR4.313	ABR4.314	ABR4.315	ABR4.316	ABR4.317	ABR4.318	ABR4.319	ABR4.320	ABR4.321	ABR4.322	ABR4.323	ABR4.324	ABR4.325	ABR4.326	ABR4.327	ABR4.328	ABR4.329	ABR4.330	ABR4.331	ABR4.332	ABR4.333	ABR4.334	ABR4.335	ABR4.336	ABR4.337	ABR4.338	ABR4.339	ABR4.340	ABR4.341	ABR4.342	ABR4.343	ABR4.344	ABR4.345	ABR4.346	ABR4.347	ABR4.348	ABR4.349	ABR4.350	ABR4.351	ABR4.352	ABR4.353	ABR4.354	ABR4.355	ABR4.356	ABR4.357	ABR4.358	ABR4.359	ABR4.360	ABR4.361	ABR4.362	ABR4.363	ABR4.364	ABR4.365	ABR4.366	ABR4.367	ABR4.368	ABR4.369	ABR4.370	ABR4.371	ABR4.372	ABR4.373	ABR4.374	ABR4.375	ABR4.376	ABR4.377	ABR4.378	ABR4.379	ABR4.380	ABR4.381	ABR4.382	ABR4.383	ABR4.384	ABR4.385	ABR4.386	ABR4.387	ABR4.388	ABR4.389	ABR4.390	ABR4.391	ABR4.392	ABR4.393	ABR4.394	ABR4.395	ABR4.396	ABR4.397	ABR4.398	ABR4.399	ABR4.400	ABR4.401	ABR4.402	ABR4.403	ABR4.404	ABR4.405	ABR4.406	ABR4.407	ABR4.408	ABR4.409	ABR4.410	ABR4.411	ABR4.412	ABR4.413	ABR4.414	ABR4.415	ABR4.416	ABR4.417	ABR4.418	ABR4.419	ABR4.420	ABR4.421	ABR4.422	ABR4.423	ABR4.424	ABR4.425	ABR4.426	ABR4.427	ABR4.428	ABR4.429	ABR4.430	ABR4.431	ABR4.432	ABR4.433	ABR4.434	ABR4.435	ABR4.436	ABR4.437	ABR4.438	ABR4.439	ABR4.440	ABR4.441	ABR4.442	ABR4.443	ABR4.444	ABR4.445	ABR4.446	ABR4.447	ABR4.448	ABR4.449	ABR4.450	ABR4.451	ABR4.452	ABR4.453	ABR4.454	ABR4.455	ABR4.456	ABR4.457	ABR4.458	ABR4.459	ABR4.460	ABR4.461	ABR4.462	ABR4.463	ABR4.464	ABR4.465	ABR4.466	ABR4.467	ABR4.468	ABR4.469	ABR4.470	ABR4.471	ABR4.472	ABR4.473	ABR4.474	ABR4.475	ABR4.476	ABR4.477	ABR4.478	ABR4.479	ABR4.480	ABR4.481	ABR4.482	ABR4.483	ABR4.484	ABR4.485	ABR4.486	ABR4.487	ABR4.488	ABR4.489	ABR4.490	ABR4.491	ABR4.492	ABR4.493	ABR4.494	ABR4.495	ABR4.496	ABR4.497	ABR4.498	ABR4.499	ABR4.500	ABR4.501	ABR4.502	ABR4.503	ABR4.504	ABR4.505	ABR4.506	ABR4.507	ABR4.508	ABR4.509	ABR4.510	ABR4.511	ABR4.512	ABR4.513	ABR4.514	ABR4.515	ABR4.516	ABR4.517	ABR4.518	ABR4.519	ABR4.520	ABR4.521	ABR4.522	ABR4.523	ABR4.524	ABR4.525	ABR4.526	ABR4.527	ABR4.528	ABR4.529	ABR4.530	ABR4.531	ABR4.532	ABR4.533	ABR4.534	ABR4.535	ABR4.536	ABR4.537	ABR4.538	ABR4.539	ABR4.540	ABR4.541	ABR4.542	ABR4.543	ABR4.544	ABR4.545	ABR4.546	ABR4.547	ABR4.548	ABR4.549	ABR4.550	ABR4.551	ABR4.552	ABR4.553	ABR4.554	ABR4.555	ABR4.556	ABR4.557	ABR4.558	ABR4.559	ABR4.560	ABR4.561	ABR4.562	ABR4.563	ABR4.564	ABR4.565	ABR4.566	ABR4.567	ABR4.568	ABR4.569	ABR4.570	ABR4.571	ABR4.572	ABR4.573	ABR4.574	ABR4.575	ABR4.576	ABR4.577	ABR4.578	ABR4.579	ABR4.580	ABR4.581	ABR4.582	ABR4.583	ABR4.584	ABR4.585	ABR4.586	ABR4.587	ABR4.588	ABR4.589	ABR4.590	ABR4.591	ABR4.592	ABR4.593	ABR4.594	ABR4.595	ABR4.596	ABR4.597	ABR4.598	ABR4.599	ABR4.600	ABR4.601	ABR4.602	ABR4.603	ABR4.604	ABR4.605	ABR4.606	ABR4.607	ABR4.608	ABR4.609	ABR4.610	ABR4.611	ABR4.612	ABR4.613	ABR4.614	ABR4.615	ABR4.616	ABR4.617	ABR4.618	ABR4.619	ABR4.620	ABR4.621	ABR4.622	ABR4.623	ABR4.624	ABR4.625	ABR4.626	ABR4.627	ABR4.628	ABR4.629	ABR4.630	ABR4.631	ABR4.632	ABR4.633	ABR4.634	ABR4.635	ABR4.636	ABR4.637	ABR4.638	ABR4.639	ABR4.640	ABR4.641	ABR4.642	ABR4.643	ABR4.644	ABR4.645	ABR4.646	ABR4.647	ABR4.648	ABR4.649	ABR4.650	ABR4.651	ABR4.652	ABR4.653	ABR4.654	ABR4.655	ABR4.656	ABR4.657	ABR4.658	ABR4.659	ABR4.660	ABR4.661	ABR4.662	ABR4.663	ABR4.664	ABR4.665	ABR4.666	ABR4.667	ABR4.668	ABR4.669	ABR4.670	ABR4.671	ABR4.672	ABR4.673	ABR4.674	ABR4.675	ABR4.676	ABR4.677	ABR4.678	ABR4.679	ABR4.680	ABR4.681	ABR4.682	ABR4.683	ABR4.684	ABR4.685	ABR4.686	ABR4.687	ABR4.688	ABR4.689	ABR4.690	ABR4.691	ABR4.692	ABR4.693	ABR4.694	ABR4.695	ABR4.696	ABR4.697	ABR4.698	ABR4.699	ABR4.700	ABR4.701	ABR4.702	ABR4.703	ABR4.704	ABR4.705	ABR4.706	ABR4.707	ABR4.708	ABR4.709	ABR4.710	ABR4.711	ABR4.712	ABR4.713	ABR4.714	ABR4.715	ABR4.716	ABR4.717	ABR4.718	ABR4.719	ABR4.720	ABR4.721	ABR4.722	ABR4.723	ABR4.724	ABR4.725	ABR4.726	ABR4.727	ABR4.728	ABR4.729	ABR4.730	ABR4.731	ABR4.732	ABR4.733	ABR4.734	ABR4.735	ABR4.736	ABR4.737	ABR4.738	ABR4.739	ABR4.740	ABR4.741	ABR4.742	ABR4.743	ABR4.744	ABR4.745	ABR4.746	ABR4.747	ABR4.748	ABR4.749	ABR4.750	ABR4.751	ABR4.752	ABR4.753	ABR4.754	ABR4.755	ABR4.756	ABR4.757	ABR4.758	ABR4.759	ABR4.760	ABR4.761	ABR4.762	ABR4.763	ABR4.764	ABR4.765	ABR4.766	ABR4.767	ABR4.768	ABR4.769	ABR4.770	ABR4.771	ABR4.772	ABR4.773	ABR4.774	ABR4.775	ABR4.776	ABR4.777	ABR4.778	ABR4.779	ABR4.780	ABR4.781	ABR4.782	ABR4.783	ABR4.784	ABR4.785	ABR4.786	ABR4.787	ABR4.788	ABR4.789	ABR4.790	ABR4.791	ABR4.792	ABR4.793	ABR4.794	ABR4.795	ABR4.796	ABR4.797	ABR4.798	ABR4.799	ABR4.800	ABR4.801	ABR4.802	ABR4.803	ABR4.804	ABR4.805	ABR4.806	ABR4.807	ABR4.808	ABR4.809	ABR4.810	ABR4.811	ABR4.812	ABR4.813	ABR4.814	ABR4.815	ABR4.816	ABR4.817	ABR4.818	ABR4.819	ABR4.820	ABR4.821	ABR4.822	ABR4.823	ABR4.824	ABR4.825	ABR4.826	ABR4.827	ABR4.828	ABR4.829	ABR4.830	ABR4.831	ABR4.832	ABR4.833	ABR4.834	ABR4.835	ABR4.836	ABR4.837	ABR4.838	ABR4.839	ABR4.840	ABR4.841	ABR4.842	ABR4.843	ABR4.844	ABR4.845	ABR4.846	ABR4.847	ABR4.848	ABR4.849	ABR4.850	ABR4.851	ABR4.852	ABR4.853	ABR4.854	ABR4.855	ABR4.856	ABR4.857	ABR4.858	ABR4.859	ABR4.860	ABR4.861	ABR4.862	ABR4.863	ABR4.864	ABR4.865	ABR4.866	ABR4.867	ABR4.868	ABR4.869	ABR4.870	ABR4.871	ABR4.872	ABR4.873	ABR4.874	ABR4.875	ABR4.876	ABR4.877	ABR4.878	ABR4.879	ABR4.880	ABR4.881	ABR4.882	ABR4.883	ABR4.884	ABR4.885	ABR4.886	ABR4.887	ABR4.888	ABR4.889	ABR4.890	ABR4.891	ABR4.892	ABR4.893	ABR4.894	ABR4.895	ABR4.896	ABR4.897	ABR4.898	ABR4.899	ABR4.900	ABR4.901	ABR4.902	ABR4.903	ABR4.904	ABR4.905	ABR4.906	ABR4.907	ABR4.908	ABR4.909	ABR4.910	ABR4.911	ABR4.912	ABR4.913	ABR4.914	ABR4.915	ABR4.916	ABR4.917	ABR4.918	ABR4.919	ABR4.920	ABR4.921	ABR4.922	ABR4.923	ABR4.924	ABR4.925	ABR4.926	ABR4.927	ABR4.928	ABR4.929	ABR4.930	ABR4.931	ABR4.932	ABR4.933	ABR4.934	ABR4.935	ABR4.936	ABR4.937	ABR4.938	ABR4.939	ABR4.940	ABR4.941	ABR4.942	ABR4.943	ABR4.944	ABR4.945	ABR4.946	ABR4.947	ABR4.948	ABR4.949	ABR4.950	ABR4.951	ABR4.952	ABR4.953	ABR4.954	ABR4.955	ABR4.956	ABR4.957	ABR4.958	ABR4.959	ABR4.960	ABR4.961	ABR4.962	ABR4.963	ABR4.964	ABR4.965	ABR4.966	ABR4.967	ABR4.968	ABR4.969	ABR4.970	ABR4.971	ABR4.972	ABR4.973	ABR4.974	ABR4.975	ABR4.976	ABR4.977	ABR4.978	ABR4.979	ABR4.980	ABR4.981	ABR4.982	ABR4.983	ABR4.984	ABR4.985	ABR4.986	ABR4.987	ABR4.988	ABR4.989	ABR4.990	ABR4.991	ABR4.992	ABR4.993	ABR4.994	ABR4.995	ABR4.996	ABR4.997	ABR4.998	ABR4.999	ABR4.1000
PCGENE	1971-17144	Prokaryotic Sequences	ABR4.1	ABR4.2	ABR4.3	ABR4.4	ABR4.5	ABR4.6	ABR4.7	ABR4.8	ABR4.9	ABR4.10	ABR4.11	ABR4.12	ABR4.13	ABR4.14	ABR4.15	ABR4.16	ABR4.17	ABR4.18	ABR4.19	ABR4.20	ABR4.21	ABR4.22	ABR4.23	ABR4.24	ABR4.25	ABR4.26	ABR4.27	ABR4.28	ABR4.29	ABR4.30	ABR4.31	ABR4.32	ABR4.33	ABR4.34	ABR4.35	ABR4.36	ABR4.37	ABR4.38	ABR4.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	

PCGENE	10711714	Prokaryotic Sequences	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6
FILE NAME	PROTEIN	ORGANISM	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6
P0HGB BACQE	GLUCOSE 1-DEHYDROGENASE B	BACILLUS MEGATERIUM	27-57					
P0HGB ECOLI	GLUCOSE DEHYDROGENASE	ESCHERICHIA COLI	434-463					
P0HRI ETRVN	KETOLACTYL REDUCTASE I	STREPTOMYCES VIOLACEOLIBER	168-195					
P0HLE BACST	LEVULINE DEHYDROGENASE	BACILLUS STEAROTHERIOPHILUS	192-219					
P0HLO AGRT4	D-LYSINE DEHYDROGENASE	AGROBACTERIUM TUMEFACIENS	117-144					
P0HAI METEX	METHANOL DEHYDROGENASE SUBUNIT 1 PREC	METHYLOBACTERIUM EXTORQUENS	133-167					
P0HAI METEX	METHANOL DEHYDROGENASE SUBUNIT 1 PREC	METHYLOBACTERIUM ORGANOPHILUM	151-167					
P0HAI JADE	METHANOL DEHYDROGENASE SUBUNIT 1 PREC	PANACOCUS DENTIFICANS	191-212					
P0HNA BACSP	NADH DEHYDROGENASE	BACILLUS SP	284-314					
P0HNA ECOLI	NADH DEHYDROGENASE	ESCHERICHIA COLI	180-214					
P0HNA BACCH	HOMOGENE DEHYDROGENASE	BACILLUS SUBTILIS	71-107	408-433				
P0HNA BACCH	HOMOGENE DEHYDROGENASE	CORYNEBACTERIUM GLUTAMICUM	105-132					
P0HNA BACCH	HOMOGENE DEHYDROGENASE	BACILLUS SPHARICUS	212-239					
P0HNA BACCH	PHENYLALANINE DEHYDROGENASE	ESCHERICHIA COLI	482-512					
P0HNA ECOLI	SUCC DEHYDROGENASE FLAVOPROTEIN SUBUNIT	ANABACNA CYLINDRICA	86-113	130-168				
P0HSS ANACV	SOLUBLE HYDROGENASE, SMALL SUBUNIT	SYNECHOCOCCUS SP	123-160					
P0HSS SYNP1	SOLUBLE HYDROGENASE, SMALL SUBUNIT	METHYLOPHILUS METHYLOPHILUS	519-466					
P0HNA ECOLI	TRIMETHYLAMINE DEHYDROGENASE	ESCHERICHIA COLI	364-611					
P0HNA ECOLI	PROBABLE ATP-DEPENDENT HELICASE DING	BACILLUS SUBTILIS	14-43	114-141				
P0HNA BACSU	DIVISION INITIATION PROTEIN	PSEUDOMONAS PUTIDA	91-120					
P0HNA BACSU	DIVISION INITIATION PROTEIN	ALZOTOBACTER VINELANDII	18-45	374-276				
P0HNA BACSU	DIVISION INITIATION PROTEIN	BACILLUS STEAROTHERIOPHILUS	82-124					
P0HNA BACSU	DIVISION INITIATION PROTEIN	BACILLUS SUBTILIS	108-135					
P0HNA BACSU	DIVISION INITIATION PROTEIN	ESCHERICHIA COLI	124-151	323-375				
P0HNA BACSU	DIVISION INITIATION PROTEIN	PSEUDOMONAS FLUORESCENS	61-90					
P0HNA BACSU	DIVISION INITIATION PROTEIN	BACILLUS SUBTILIS	497-524	548-581				
P0HNA BACSU	DIVISION INITIATION PROTEIN	BACILLUS SUBTILIS	418-483					
P0HNA BACSU	DIVISION INITIATION PROTEIN	BACILLUS SUBTILIS	116-140					
P0HNA BACSU	DIVISION INITIATION PROTEIN	BORRELLIA BURGDORFERI	182-216	248-275	341-387	436-461		
P0HNA BACSU	DIVISION INITIATION PROTEIN	BORRELLIA BURGDORFERI	71-100	111-118	353-360			
P0HNA BACSU	DIVISION INITIATION PROTEIN	ESCHERICHIA COLI	164-400					
P0HNA BACSU	DIVISION INITIATION PROTEIN	MICROCOCCUS LUTEUS	181-415					
P0HNA BACSU	DIVISION INITIATION PROTEIN	MICROCOCCUS LUTEUS	8-56	75-112	274-310	350-389		
P0HNA BACSU	DIVISION INITIATION PROTEIN	MYCOPLASMA CAPRICOLUM	163-199					
P0HNA BACSU	DIVISION INITIATION PROTEIN	PROTEUS MIRABILIS	198-419					
P0HNA BACSU	DIVISION INITIATION PROTEIN	PSEUDOMONAS PUTIDA	43-72	36-110	165-180			
P0HNA BACSU	DIVISION INITIATION PROTEIN	SPYROPLASMA CITRI	312-353					
P0HNA BACSU	DIVISION INITIATION PROTEIN	CHLAMYDIA TRACHOMATIS	82-109					
P0HNA BACSU	DIVISION INITIATION PROTEIN	ESCHERICHIA COLI	82-109					
P0HNA BACSU	DIVISION INITIATION PROTEIN	SALMONELLA TYPHIMURUM	146-190					
P0HNA BACSU	DIVISION INITIATION PROTEIN	ESCHERICHIA COLI	487-524	548-581				
P0HNA BACSU	DIVISION INITIATION PROTEIN	BORRELLIA BURGDORFERI	312-394					
P0HNA BACSU	DIVISION INITIATION PROTEIN	BACILLUS MEGATERIUM	248-275	312-346				
P0HNA BACSU	DIVISION INITIATION PROTEIN	BRUCELLA OVIS	561-588					
P0HNA BACSU	DIVISION INITIATION PROTEIN	CALOBACTER CRESCENTUS	499-526					
P0HNA BACSU	DIVISION INITIATION PROTEIN	CLOSTRIDIUM ACETOBUTYLICUM	496-537					
P0HNA BACSU	DIVISION INITIATION PROTEIN	CLOSTRIDIUM PERFRINGENS	527-539					
P0HNA BACSU	DIVISION INITIATION PROTEIN	METHANOCALDOCoccus MAZEI	502-539					
P0HNA BACSU	DIVISION INITIATION PROTEIN	MYCOBACTERIUM TUBERCULOSIS	43-72	533-572				
P0HNA BACSU	DIVISION INITIATION PROTEIN	STREPTOMYCES COELICOLOR	114-141					
P0HNA BACSU	DIVISION INITIATION PROTEIN	ESCHERICHIA COLI	518-512					
P0HNA BACSU	DIVISION INITIATION PROTEIN	ZYTHOMONAS MOBILIS	74-51					
P0HNA BACSU	DIVISION INITIATION PROTEIN	STREPTOMYCES PEUCETIUS	104-172					
P0HNA BACSU	DIVISION INITIATION PROTEIN	SUBLOBLOUS SOLFAERICUS	58-85	417-444	1382-1416			
P0HNA BACSU	DIVISION INITIATION PROTEIN	BACILLUS SUBTILIS	71-104					
P0HNA BACSU	DIVISION INITIATION PROTEIN	ESCHERICHIA COLI	310-351					
P0HNA BACSU	DIVISION INITIATION PROTEIN	SACCHAROPOLYSPOREA ERYTHRAEA						

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PGCENE	10117184	Frishartjele Segments	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7
VILLE NAME	PHUTIN	ORGANISM	21-16						AREA.7
POSSIBLE PROTEIN 1 END		STAPHYLOCOCCUS AUREUS	4-11						AREA.7
FERREDOXIN-NADP REDUCTASE		SYNECHOCOCCUS SP	176-201						
FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEP		ESCHERICHIA COLI	182-214	281-308					
FERRIC ENTEROBACTIN TRANSPORT PROTEIN FEP		ESCHERICHIA COLI	128-155						
FERREDOXIN, HETERODICIST		ANABAENA SP	2-39						
FERREDOXIN-LIKE PROTEIN IN NIF REGION		ANABAENA SP	67-94						
FILAMENTOUS HEMAGGLUTININ		BORDETTELLA PERTUSSIS	112-118	1359-1366		2063-2114	2841-2863	1051-1085	3167-3194
HAEMOLYIN-LIKE PROTEIN FHAC PRECURSOR		BORDETTELLA PERTUSSIS	142-169						
FORMATE HYDROGENLYASE TRANSACTIVATOR		ESCHIERICHIA COLI	36-63	350-364		401-428			
FERROCHROME-IRON RECEPTOR PRECURSOR		ESCHERICHIA COLI	458-485						
PROTEIN FRIB PRECURSOR		ESCHERICHIA COLI	222-234						
OUTER-MEMBRANE RECEPTOR		ESCHERICHIA COLI	582-614						
FIBRIL PROTEIN		SPIROPLASMA CITRI	181-193	326-367					
CELL FILAMENTATION PROTEIN FIC		ESCHIERICHIA COLI	151-178						
CELL FILAMENTATION PROTEIN FIC		SALMONELLA TYPHIUMURIUM	208-235	5405-567		618-645			
OUTER MEMBRANE PROTEIN FIMC PRECURSOR		BORDETTELLA PERTUSSIS	51-78						
CHAPERONE PROTEIN FIMC PRECURSOR		ESCHERICHIA COLI	222-253	458-485					
FIMD PROTEIN PRECURSOR		ESCHERICHIA COLI	105-192			563-590			
TYPE 1 FIMBRIAL REGULATOR Y PROTEIN FIME		ESCHERICHIA COLI	49-76						
FIMBRIAL Y PROTEIN		SALMONELLA TYPHIUMURIUM	42-49	162-192		196-230			
FIMBRIAL Z PROTEIN		ESCHERICHIA COLI	175-209						
FIMBRIAL Z PROTEIN		SALMONELLA TYPHIUMURIUM	145-172						
FIMD PROTEIN		ESCHERICHIA COLI	163-189						
FIMBRIAL NUCLEI		RICKETTSIA RICKETTSII	129-156						
FIMC PROTEIN		ATOPHIZOBIIUM CAULIMODANS	227-274						
SENSOR PROTEIN FIX		ATOPHIZOBIIUM CAULIMODANS	27-34	351-380					
SENSOR PROTEIN FIX		BRADYRHIZOBIIUM JAPONICUM	8-35	371-398					
FLAGELLAR FILAMENT 1 KD CORE PROTEIN		BORDELLA BURGDORFERI	61-92	157-184					
FLAGELLIN A1 PRECURSOR		HALOBACTERIUM HALOBIIUM	36-73	113-160					
FLAGELLIN B1 PRECURSOR		METHANOCOCCUS VOLTAE	38-66						
FLAGELLIN B1 PRECURSOR		METHANOCOCCUS VOLTAE	36-63						
FLAGELLIN B1 PRECURSOR		HALOBACTERIUM HALOBIIUM	33-76	137-180					
FLAGELLIN B1 PRECURSOR		HALOBACTERIUM HALOBIIUM	36-90	154-181					
FLAGELLIN B1 PRECURSOR		HALOBACTERIUM HALOBIIUM	31-149	151-186					
FLAGELLIN B1 PRECURSOR		BACILLUS SUBTILIS	13-42	144-181					
FLAGELLIN B1 PRECURSOR		CAMPYLOBACTER COLI	226-266	310-337					
FLAGELLIN A		CAMPYLOBACTER COLI	28-42						
FLAGELLIN A		METHANOCOCCUS VOLTAE	1-41	31-88					
FLAGELLIN A PRECURSOR		PSEUDOMONAS AERUGINOSA	181-219	228-265		360-391			
FLAGELLIN		BRADYRHIZOBIIUM JAPONICUM	163-189						
FLAGELLAR FILAMENT PROTEIN PRECURSOR		SPYROCHAETA AURANTIA	35-49	219-283					
FLAGELLAR FILAMENT PROTEIN PRECURSOR		TREPONEMA HYDROSYPHANTIAE	243-270						
FLAGELLAR FILAMENT OUTER LAYER PROTEIN		TREPONEMA PALLIDUM	144-191	497-535					
FLAGELLIN B		CAMPYLOBACTER COLI	226-266	310-337					
FLAGELLIN B		CAMPYLOBACTER COLI	86-113	172-210					
FLAGELLIN B		BRADYRHIZOBIIUM JAPONICUM	18-52						
REGULATORY PROTEIN FLAY		CLOSTRIDIUM MP	291-318	551-578					
FLAGELLIN		BACILLUS SUBTILIS	102-129	228-255					
FLAGELLAR BASAL-BODY ROD PROTEIN FLOG		BACILLUS SUBTILIS	62-89						
FLAGELLAR HOOK-ASSOCIATED PROTEIN 1		SALMONELLA TYPHIUMURIUM	12-50	333-360		436-540			
FLAGELLAR HOOK-ASSOCIATED PROTEIN 2		ESCHERICHIA COLI	61-105	228-266					
FLAGELLAR HOOK-ASSOCIATED PROTEIN 3		SALMONELLA TYPHIUMURIUM	61-105	228-266					
FLAGELLAR HOOK-ASSOCIATED PROTEIN 3		ESCHERICHIA COLI	6-33						
FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLID		FLAGELLAR TRANSCRIPTIONAL ACTIVATOR	198-232						
FLAGELLAR		PSEUDOMONAS AERUGINOSA							

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EC NAME	1071744	Proteolytic Enzymes	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PRD1 ECOLI	PROTEIN	ORGANISM	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8
PRD2 ECOLI	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	ESCHERICHIA COLI	393-422							
PRD3 ECOLI	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT	WOLINELLA SUCCINOTRINIS	487-514							
PRD4 ECOLI	GLUTAMATE REDUCTASE FLAVOPROTEIN SUBUNIT	MYXOCOCCUS XANTHUS	13-42	478-505						
PRD5 ECOLI	FUMARATE-TETRAHYDROFOLATE LIGASE	CLOSTRIIDIUM THERMOPHILUM	161-190							
PRD6 ECOLI	FORMYLTRANSFERASE	METHANOBACTERIUM THERMAUTOTROPHICUS	6-43							
PRD7 ECOLI	CELL DIVISION PROTEIN FTS	BACILLUS SUBTILIS	36-110							
PRD8 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	301-338	375-418						
PRD9 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	6-31							
PRD10 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	61-90							
PRD11 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	151-188							
PRD12 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	378-395							
PRD13 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	216-260							
PRD14 ECOLI	CELL DIVISION PROTEIN FTS	ESCHERICHIA COLI	7-45							
PRD15 ECOLI	L-FUCOSE OPERON ACTIVATOR	ESCHERICHIA COLI	290-317							
PRD16 ECOLI	FUMARATE HYDROLYTASE CLASS I, AEROBIC	BACILLUS STEAROTHERMOPHILUS	414-445							
PRD17 ECOLI	FUMARATE HYDROLYTASE	BACILLUS SUBTILIS	92-110							
PRD18 ECOLI	FERRIC UPTAKE REGULATION PROTEIN	YERSINIA PESTIS	303-329							
PRD19 ECOLI	GLYC 3-PHOS DEHYDROGENASE A	ESCHERICHIA COLI	87-114							
PRD20 ECOLI	GLYC 3-PHOS DEHYDROGENASE 2	ANABAENA VARIABILIS	162-189							
PRD21 ECOLI	GLYC 3-PHOS DEHYDROGENASE 3	ANABAENA VARIABILIS	216-224							
PRD22 ECOLI	GLYC 3-PHOS DEHYDROGENASE C	ESCHERICHIA COLI	46-76	227-271						
PRD23 ECOLI	GLYC 3-PHOS DEHYDROGENASE	BACILLUS MEGATERIUM	49-76							
PRD24 ECOLI	GLYC 3-PHOS DEHYDROGENASE	BACILLUS SUBTILIS	259-286							
PRD25 ECOLI	GLYC 3-PHOS DEHYDROGENASE	PYROCOCCUS WOESSEI	290-328							
PRD26 ECOLI	GLYC 3-PHOS DEHYDROGENASE	THELAMOTOGA MARITIMA	101-143	241-269						
PRD27 ECOLI	GLUCOSE-4-PHOSPHATE ISOMERASE B	BACILLUS STEAROTHERMOPHILUS	301-328							
PRD28 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ESCHERICHIA COLI	163-193							
PRD29 ECOLI	GLUCOSE-4-PHOSPHATE 1-DEHYDROGENASE	ZYMONOMAS MOBILIS	178-203							
PRD30 ECOLI	CYANIDE CONTROL PROTEIN	PSEUDOMONAS FLUORESCENS	86-113							
PRD31 ECOLI	GALACTONASE	SALMONELLA TYPHIMURUM	124-158	219-269						
PRD32 ECOLI	GAL-1-PHOS UNIDITYLTRANSFERASE	HAEMOPHILUS INFLUENZAE	304-338							
PRD33 ECOLI	GAL-1-PHOS UNIDITYLTRANSFERASE	LACTOBACILLUS HELVETICUS	51-91							
PRD34 ECOLI	GALACTOSE OPERON REPRESSOR	SALMONELLA TYPHIMURUM	181-209							
PRD35 ECOLI	GALACTOSE OPERON REPRESSOR	HAEMOPHILUS INFLUENZAE	351-278							
PRD36 ECOLI	DE-GALACTOSE 1-DEHYDROGENASE	PSEUDOMONAS FLUORESCENS	78-105							
PRD37 ECOLI	GTP CYCLOHYDROLASE II	ESCHERICHIA COLI	197-227	246-273						
PRD38 ECOLI	GTP CYCLOHYDROLASE II	PHOTOBACTERIUM LEIGNATHI	10-37							
PRD39 ECOLI	GLYCINE CLEAVAGE SYSTEM H PROTEIN	ESCHERICHIA COLI	216-246							
PRD40 ECOLI	GLYCINE DEHYDROGENASE	ESCHERICHIA COLI	60-94							
PRD41 ECOLI	GLYCINE CLEAVAGE SYSTEM TRANSACTIVATOR	ESCHERICHIA COLI	34-51							
PRD42 ECOLI	PROTEIN K	ESCHERICHIA COLI	46-83	182-216	350-384					
PRD43 ECOLI	SPORE GERMINATION PROTEIN I	BACILLUS SUBTILIS	293-323							
PRD44 ECOLI	SPORE GERMINATION PROTEIN III PRECURSOR	BACILLUS SUBTILIS	13-40							
PRD45 ECOLI	GERMINATION PROTEIN GENE	BACILLUS SUBTILIS	6-33							
PRD46 ECOLI	ANTIBACTERIAL PROTEIN 2	STAPHYLOCOCCUS HAEMOLYTICUS	398-423							
PRD47 ECOLI	ANTIBACTERIAL PROTEIN 3	STAPHYLOCOCCUS HAEMOLYTICUS	531-568							
PRD48 ECOLI	GLUCOSE INHIBITED DIVISION PROTEIN A	BACILLUS SUBTILIS	539-566							
PRD49 ECOLI	GLUCOSE INHIBITED DIVISION PROTEIN A	ESCHERICHIA COLI	34-41							
PRD50 ECOLI	GLUCOSE INHIBITED DIVISION PROTEIN A	PSEUDOMONAS PUTIDA	25-52							
PRD51 ECOLI	GLUCOSE INHIBITED DIVISION PROTEIN B	BACILLUS SUBTILIS	328-372							
PRD52 ECOLI	GLUCOSE INHIBITED DIVISION PROTEIN B	PSEUDOMONAS PUTIDA	20-79							
PRD53 ECOLI	GLUCOSE TRANSPORT PROTEIN	SYNCHOCYSTIS SP	114-141							
PRD54 ECOLI	GLYCEROL DEHYDROGENASE	BACILLUS STEAROTHERMOPHILUS	209-243							
PRD55 ECOLI	GLYCEROL SYNTHASE	ESCHERICHIA COLI	18-45							
PRD56 ECOLI	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE	ESCHERICHIA COLI								
PRD57 ECOLI	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE	SALMONELLA TYPHIMURUM								
PRD58 ECOLI	GLUC-4-PHOS-4-PHOSAMINOTRANSFERASE	ESCHERICHIA COLI								
PRD59 ECOLI	GLN-LIKE PROTEIN I	METHANOCOCCUS THERMOTROPHICUS								

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PGCENE	1017114	Proteomic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILENAME	PROTEIN	ORGANISM	210-217								
PGSP1_XANCP	PROTEIN F	XANTHOMONAS CAMPESTRIS	18-39								
PGSP1_PSEAE	PROTEIN H PRECURSOR	PSEUDOMONAS AERUGINOSA	37-41								
PGSP1_AENHY	PROTEIN I PRECURSOR	AEROMONAS HYDROPHILA	31-43								
PGSP1_EAWCA	PROTEIN J PRECURSOR	ERWINIA CAROTOVORA	140-147								
PGSP1_KLEPN	PROTEIN K	KLEBSIELLA PNEUMONIAE	78-113								
PGSP1_EAWCA	PROTEIN K	ERWINIA CAROTOVORA	78-113								
PGSP1_EAWCH	PROTEIN K	ERWINIA CHRYSAEANTHEAE	78-113								
PGSP1_KLEPN	PROTEIN K	KLEBSIELLA PNEUMONIAE	72-99								
PGSP1_PSEAE	PROTEIN K	PSEUDOMONAS AERUGINOSA	362-289								
PGSP1_EAWCH	PROTEIN L	ERWINIA CHRYSAEANTHEAE	1-43	348-384	371-378						
PGSP1_EAWCH	PROTEIN L	ERWINIA CHRYSAEANTHEAE	18-73	397-323							
PGSP1_EAWCA	PROTEIN M	XANTHOMONAS CAMPESTRIS	108-145								
PGSP1_EAWCH	PROTEIN D PRECURSOR	ERWINIA CHRYSAEANTHEAE	239-262	448-475	546-573	637-484					
PGSP1_STRDO	GLYCOSYLTRANSFERASE-1 PRECURSOR	STREPTOCOCCUS DOWNEI	177-204	312-239	644-491	1182-1416	1495-1379				
PGSP1_STRDO	GLYCOSYLTRANSFERASE-1 PRECURSOR	STREPTOCOCCUS DOWNEI	171-199	306-211	418-483	1182-1412	1495-1379				
PGSP1_STRDO	GLYCOSYLTRANSFERASE-1 PRECURSOR	STREPTOCOCCUS MUTANS	297-350								
PGSP1_STRDO	GLYCOSYLTRANSFERASE-1 PRECURSOR	STREPTOCOCCUS MUTANS	42-93	110-137	161-188	199-246	313-347	592-637			
PGSP1_STRDO	GLYCOSYLTRANSFERASE-1 PRECURSOR	STREPTOCOCCUS MUTANS	4-49	110-138	233-262	370-361	614-653				
PGSP1_STRDO	GLYCOSYLTRANSFERASE-1 PRECURSOR	STREPTOCOCCUS DOWNEI	273-316	418-463	1281-1315						
PGSP1_METTP	POSSIBLE G-T MISMATCHES REPAIR ENZYME	METHANOBACTERIUM THERMOPHILICUM	80-107	148-175							
PGSP1_ECOLI	GMP SYNTHASE	BACILLUS SUBTILIS	314-348	399-436	478-505						
PGSP1_ECOLI	GMP SYNTHASE	ESCHERICHIA COLI	105-132								
PGSP1_BACCI	BETA-GLUCANASE PRECURSOR	BACILLUS CIRCULANS	164-191								
PGSP1_BACCI	BETA-GLUCANASE PRECURSOR	BACILLUS LICHENIFORMIS	132-166								
PGSP1_BACCI	BETA-GLUCANASE PRECURSOR	BACILLUS MACERANS	326-360								
PGSP1_BACCI	ENDOGALACTANASE A	BACILLUS SP	18-49								
PGSP1_BACCI	ENDOGALACTANASE PRECURSOR	BACILLUS SUBTILIS	270-304	376-403							
PGSP1_BUTTH	ENDOGALACTANASE 1	BUTYRIVIBRIO FIBRISOLVENS	154-181	432-465							
PGSP1_BACCI	ENDOGALACTANASE E-3 PRECURSOR	THELAMONOSPORA FUSCA	301-328								
PGSP1_BACCI	ENDOGALACTANASE C PRECURSOR	BACILLUS SP	110-137	348-378	518-565						
PGSP1_BACCI	ENDOGALACTANASE 1 PRECURSOR	BACILLUS SUBTILIS	270-304								
PGSP1_BACCI	ENDOGALACTANASE 1 PRECURSOR	FIBROBACTER SUCCINOGENES	542-586								
PGSP1_THIEFU	ENDOGALACTANASE E-4 PRECURSOR	THELAMONOSPORA FUSCA	308-342								
PGSP1_THIEFU	ENDOGALACTANASE E-3 PRECURSOR	THELAMONOSPORA FUSCA	44-71								
PGSP1_BACCI	ENDOGALACTANASE A PRECURSOR	BACILLUS LAUTUS	410-437	436-481							
PGSP1_CLOTH	ENDOGALACTANASE A PRECURSOR	CLOSTRIDIUM THERMOCELLUM	334-384								
PGSP1_PSEPL	ENDOGALACTANASE A PRECURSOR	PSEUDOMONAS FLUORESCENS	762-789								
PGSP1_RUMAL	ENDOGALACTANASE A	RUMINOCOCCUS ALBUS	394-321								
PGSP1_RUMAL	CELLULOXYNASE A	RUMINOCOCCUS FLAVIFACIENS	376-303								
PGSP1_BACCI	ENDOGALACTANASE B PRECURSOR	BACILLUS LAUTUS	371-450								
PGSP1_CALSA	ENDOGALACTANASE B	CALDOCELLUM SACCHAROLYTICUM	151-182	444-478							
PGSP1_CELFI	ENDOGALACTANASE B PRECURSOR	CELLULOMONAS FIMI	266-293								
PGSP1_CLOCL	ENDOGALACTANASE B PRECURSOR	CLOSTRIDIUM CELLULOVORANS	144-171	266-300							
PGSP1_CLOTH	ENDOGALACTANASE B PRECURSOR	CLOSTRIDIUM THERMOCELLUM	514-541								
PGSP1_CELFI	ENDOGALACTANASE C PRECURSOR	CELLULOMONAS FIMI	881-908								
PGSP1_PSEPL	ENDOGALACTANASE C PRECURSOR	PSEUDOMONAS FLUORESCENS	53-83								
PGSP1_CLOCL	ENDOGALACTANASE D PRECURSOR	CLOSTRIDIUM CELLULOVYTICUM	312-453								
PGSP1_CLOTH	ENDOGALACTANASE D PRECURSOR	CLOSTRIDIUM THERMOCELLUM	145-172	271-398							
PGSP1_CLOTH	ENDOGALACTANASE E PRECURSOR	CLOSTRIDIUM THERMOCELLUM	158-185	207-234	284-311						
PGSP1_CLOTH	ENDOGALACTANASE H PRECURSOR	CLOSTRIDIUM THERMOCELLUM	46-73	423-452							
PGSP1_EAWCA	ENDOGALACTANASE PRECURSOR	ERWINIA CAROTOVORA	70-47	113-149							
PGSP1_CLOTH	MUTATIVE ENDOGLUCANASE X	CLOSTRIDIUM THERMOCELLUM	101-139								
PGSP1_CLOTH	ENDOGALACTANASE Z PRECURSOR	CLOSTRIDIUM THERMOCELLUM	296-326	922-540							
PGSP1_BACCI	ENDOGALACTANASE	BACILLUS POLYMYXA	199-225								
PGSP1_BACCI	ENDOGALACTANASE PRECURSOR	BACILLUS SP	321-348								
PGSP1_BACCI	ENDOGALACTANASE PRECURSOR	BACILLUS SP	188-219	301-378	637-464						

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PCGENE	1074.17814	Proteolytic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PROTEIN	1074.17814	PROTEIN	100-317	237-291							AREA1
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA2
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA3
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA4
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA5
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA6
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA7
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA8
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA9
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA10
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA11
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA12
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA13
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA14
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA15
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA16
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA17
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA18
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA19
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA20
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA21
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA22
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA23
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA24
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA25
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA26
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA27
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA28
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA29
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA30
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA31
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA32
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA33
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA34
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA35
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA36
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA37
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA38
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA39
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA40
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA41
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA42
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA43
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA44
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA45
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA46
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA47
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA48
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA49
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA50
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA51
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA52
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA53
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA54
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA55
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA56
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA57
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA58
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA59
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA60
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA61
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA62
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA63
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA64
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA65
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA66
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA67
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA68
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA69
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA70
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA71
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA72
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA73
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA74
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA75
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA76
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA77
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA78
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA79
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA80
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA81
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA82
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA83
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA84
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA85
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA86
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA87
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA88
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA89
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA90
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA91
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA92
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA93
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA94
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA95
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA96
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA97
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA98
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA99
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA100
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA101
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA102
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA103
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA104
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA105
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA106
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA107
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA108
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA109
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA110
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA111
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA112
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA113
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA114
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA115
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA116
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA117
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA118
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA119
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA120
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA121
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA122
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA123
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA124
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA125
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA126
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA127
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA128
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA129
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA130
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA131
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA132
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA133
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA134
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA135
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA136
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA137
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA138
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA139
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA140
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA141
ALPHA CHAIN	ALPHA CHAIN	ALPHA CHAIN	100-317	237-291							AREA142
BETA CHAIN	BETA CHAIN	BETA CHAIN	100-317	237-291							AREA143
ALPHA CHAIN	AL										

[illegible]

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[illegible]

PCCLP	101176.4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
ELLIPSE	PROTEIN	ORGANISMI	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PHIM BRAJA	BIOSYNTHESIS PROTEIN NIEN	BRADYRHIZOBIUM JAPONICUM	116-166								
PHIS ANAS	NIH3 PROTEIN	ANABAENA SP	112-139								
PHIS LACDE	NIH3 PROTEIN HOMOLOG	LACTOBACILLUS DELBRUECKII	59-86								
PHIT AZOVI	NIH7 PROTEIN	AZOTOBACTER VINELANDII	6-33								
PHIU ANASL	NIH10 PROTEIN	ANABAENA SP	7-69								
PHIU ANAS	NIH10 PROTEIN	ANABAENA SP	148-178								
PHIU KLEPH	NIH10 PROTEIN	KLERSIELLA PNEUMONIAE	66-93								
PHIK ECOLI	NICKEL TRANSPORT PROTEIN NIK A PRECURSOR	ESCHERICHIA COLI	122-149								
PHIK ECOLI	NICKEL TRANSPORT PROTEIN NIK E	ESCHERICHIA COLI	177-204								
PHIB ECOLI	NITRATE REDUCTASE	ESCHERICHIA COLI	345-372								
PHIC ECOLI	NIH3 PROTEIN	ESCHERICHIA COLI	212-239								
PHIS PSEST	PSEUDOMONAS CYTOCHROME OXIDASE PRECURSOR	PSEUDOMONAS STUTZERI	303-333								
PHIB LACLA	117 KD MEMBRANE ASSOCIATED PROTEIN	LACTOCOCCUS LACTIS	302-339								
PHIS LACLA	NISIN BIOSYNTHESIS PROTEIN MISC	LACTOCOCCUS LACTIS	32-92								
PHIS LACLA	NISIN TRANSPORT PROTEIN MISC	LACTOCOCCUS LACTIS	223-233								
PHIV CLOPA	HOMOCITRATE SYNTHASE, ALPHA SUBUNIT	CLOSTRIDIUM PASTEURIANUM	100-127								
PHIV CLOPA	HOMOCITRATE SYNTHASE, OMEGA SUBUNIT	CLOSTRIDIUM PASTEURIANUM	63-94								
PHIV ECOLI	FOUR PROTEIN MDC PRECURSOR	ESCHERICHIA COLI	32-49								
PHIC BRASP	MODULATION PROTEIN C	BRADYRHIZOBIUM SP	3-30								
PHIC RHELO	MODULATION PROTEIN C	RHIZOBIUM LOTI	286-313								
PHIC RHELO	MODULATION PROTEIN C	RHIZOBIUM LEGUMINOSARUM	14-48								
PHIC RHELO	MODULATION PROTEIN F	RHIZOBIUM LEGUMINOSARUM	31-58								
PHIC RHELO	MODULATION PROTEIN F	RHIZOBIUM MELILOTI	39-66								
PHIC RHELO	MODULATION PROTEIN F	RHIZOBIUM MELILOTI	8-33								
PHIC RHELO	MODULATION PROTEIN G	RHIZOBIUM MELILOTI	26-33								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	60-87								
PHIC RHELO	MODULATION PROTEIN D	BRADYRHIZOBIUM SP	104-134								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM LEGUMINOSARUM	364-391								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	355-382								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	420-454								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	418-443								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	739-766								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	232-259								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	131-160								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	88-113								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	179-246								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	137-154								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	267-294								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	552-591								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	112-147								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	317-344								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	187-228								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	107-134								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	4-45								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	125-153								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	91-123								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	319-346								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	72-111								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	109-136								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	53-79								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	65-92								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	44-91								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	67-94								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	194-223								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	35-412								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	431-478								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	80-107								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	37-34								
PHIC RHELO	MODULATION PROTEIN D	RHIZOBIUM MELILOTI	616-641								

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PCGENE	10711784	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PHIC LISMO	PHOSPHOLIPASE C PRECURSOR	LISTERIA MONOCYTOGENES	147-174								
PHIC PSEAE	HEMOLYTIC PHOSPHOLIPASE C PRECURSOR	PSEUDOMONAS AERUGINOSA	615-712								
PHIC STAAU	PHOSPHOLIPASE C PRECURSOR	STAPHYLOCOCCUS AUREUS	6-13								
PHILD BACCE	PHOSPHOLIPASE C PRECURSOR	BACILLUS CEREUS	179-206								
PHIL LEPIN	SPHINGOMYELINASE C PRECURSOR	LEPTOSPIRA INTEROGANS	10-37		104-128						
PHIND ECOLI	PIIND PROTEIN	ESCHERICHIA COLI	296-326								
PHINK ECOLI	PIIND PROTEIN	ESCHERICHIA COLI	178-205								
PHINN ECOLI	PIIND PROTEIN	ESCHERICHIA COLI	5-35								
PHIOE CITFA	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	CITROBACTER FREUNDII	13-40		42-103						
PHIOE ECOLI	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	ESCHERICHIA COLI	13-40		64-103						
PHIOE KLEOX	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	KLEBSIELLA OXYTOCA	13-40		64-91						
PHIOE KLEPN	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	KLEBSIELLA PNEUMONIAE	13-40		64-103						
PHIOE SALTU	OUTER MEMBRANE PORE PROTEIN E PRECURSOR	SALMONELLA TYPHIMURUM	61-104		110-147						
PHIOF BACSU	ALK PHOS SYNTHESIS TRANS REG PROTEIN	BACILLUS SUBTILIS	182-219								
PHIOQ ECOLI	SENSOR PROTEIN PHOQ	ESCHERICHIA COLI	244-278								
PHIOQ SALTU	VIOLUENCE SENSOR PROTEIN PHOQ	SALMONELLA TYPHIMURUM	226-260								
PHIOH BACSU	ALK PHOS SYNTHESIS SENSOR PROTEIN PHIOH	BACILLUS SUBTILIS	99-143		187-423						
PHIOA ECOLI	PHOTOREPAIR PROTEIN PHIA	ESCHERICHIA COLI	61-90		107-141						
PHIOA STNPP	R-PHYCOCYANIN II ALPHA CHAIN	SYNECHOCOCCUS SP	30-43								
PHIOA STNPP	R-PHYCOCYANIN II ALPHA CHAIN	SYNECHOCOCCUS SP	30-43								
PHIOA ECOLI	GLYCOCEN PHOSPHORYLASE	ESCHERICHIA COLI	20-47		48-113						
PHIOA ECOLI	MALTODEXTRIN PHOSPHORYLASE	ESCHERICHIA COLI	71-108								
PHIOA ECOLI	PROB SIGNAL RECOGNITION PARTICLE PROTEIN	NEISSERIA GONORRHOEA	17-48								
PHIOA ECOLI	FIABRIAL ASSEMBLY PROTEIN PILB	PSEUDOMONAS AERUGINOSA	16-60								
PHIOA ECOLI	PILC PROTEIN	PSEUDOMONAS AERUGINOSA	143-170								
PHIOA ECOLI	LEADER PEPTIDASE	NEISSERIA GONORRHOEA	110-137								
PHIOA ECOLI	FIABRIAL ASSEMBLY PROTEIN PILQ PRECURSOR	PSEUDOMONAS AERUGINOSA	71-115		619-666						
PHIOA ECOLI	SENSOR PROTEIN PILS	PSEUDOMONAS AERUGINOSA	9-46								
PHIOA ECOLI	PI PROTEIN	ESCHERICHIA COLI	156-188								
PHIOA ECOLI	PILIN GENE INVERTING PROTEIN	ADONELLA BOVIS	42-89		152-182						
PHIOA ECOLI	PILIN GENE INVERTING PROTEIN	ADONELLA LACUNATA	152-182								
PHIOA ECOLI	PHOSPHODIESTERASE PRECURSOR	BACILLUS CEREUS	217-245								
PHIOA ECOLI	PHOSPHODIESTERASE PRECURSOR	BACILLUS THURINGENSIS	216-245								
PHIOA ECOLI	PHOSPHODIESTERASE PRECURSOR	LISTERIA MONOCYTOGENES	216-245								
PHIOA ECOLI	ACV TRANSFERASE	ESCHERICHIA COLI	106-133								
PHIOA ECOLI	PLSX PROTEIN	ESCHERICHIA COLI	241-270								
PHIOA ECOLI	PECTIN LYASE	ERWINIA CAROTOVORA	27-97								
PHIOA ECOLI	PMBA PROTEIN	ERWINIA CHRYSANTHEMI	60-87								
PHIOA ECOLI	PECTINESTERASE PRECURSOR	ESCHERICHIA COLI	82-316								
PHIOA ECOLI	PHOSPHOGLYCERATE MUTASE	SYNOMONAS AOBILIS	13-40		80-110						
PHIOA ECOLI	POLYTRIMONUC NUKLEOTIDYL TRANSFERASE	ESCHERICHIA COLI	240-294								
PHIOA ECOLI	PMIR: PMIR:IM	SALMONELLA TYPHIMURUM	178-203								
PHIOA ECOLI	PYRUVATE OXIDOTHIOPHOSPHATE DOKINASE	BACTEROIDES SYMBIOSIS	31-78								
PHIOA ECOLI	OUTER MEMBRANE PORIN F PRECURSOR	PSEUDOMONAS SYRINGAE	111-138								
PHIOA ECOLI	PORIN O PRECURSOR	PSEUDOMONAS AERUGINOSA	390-424								
PHIOA ECOLI	PORIN P PRECURSOR	PSEUDOMONAS AERUGINOSA	119-181		260-387	369-396					
PHIOA ECOLI	BINDING PROTEIN PRECURSOR	ESCHERICHIA COLI	326-347								
PHIOA ECOLI	PURINE: URACIL: GUANINE: ADENINE: AMPICILLIN	ESCHERICHIA COLI	61-118								
PHIOA ECOLI	PYRUVATE DEHYDROGENASE	ESCHERICHIA COLI	8-38								
PHIOA ECOLI	ALKALINE PHOSPHATASE III PRECURSOR	BACILLUS SUBTILIS	109-150		437-460						
PHIOA ECOLI	ALKALINE PHOSPHATASE IV PRECURSOR	BACILLUS SUBTILIS	85-123		378-383						
PHIOA ECOLI	ALKALINE PHOSPHATASE PRECURSOR	ESCHERICHIA COLI	332-362								
PHIOA ECOLI	ALKALINE PHOSPHATASE PRECURSOR	ESCHERICHIA FERGUSONII	334-363								
PHIOA ECOLI	PROLYL ENDOPEPTIDASE PRECURSOR	FLAVOBACTERIUM MENINGOSEPTICUM	158-199								
PHIOA ECOLI	PROLYL ENDOPEPTIDASE PRECURSOR	FLAVOBACTERIUM MENINGOSEPTICUM	158-199		334-383						
PHIOA ECOLI	PHOSPHOENOLPYRUVATE CARBOXYKINASE	ESCHERICHIA COLI	45-73								

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ECCLONE	1974174.4	Protein Sequence	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PRMA STAP	REPLICATION AND MAINTENANCE PROTEIN	STAPHYLOCOCCUS EPIDERMIDIS	3-36	81-108							
PRP1 ECCL	REPLICATION PROTEIN REPA	ESCHERICHIA COLI	30-37	90-117							
PRPA BACSU	REPA PROTEIN	BACILLUS SUBTILIS	142-173	228-255							
PRPA ECCL	REPA PROTEIN	ESCHERICHIA COLI	91-118	138-172							
PRPA RECO	REPLICATION PROTEIN	NEISSERIA GONORRHOEAE	184-211								
PRPB STAAL	REPLICATION INITIATION PROTEIN	LACTOBACILLUS PLANTARUM	354-284								
PRPB STAAL	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	350-285								
PRPB STAAL	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	438-467								
PRPB STAAL	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AGALACTIAE	427-467								
PRPB STAAL	REPLICATION INITIATION PROTEIN	STREPTOCOCCUS PYOGENES	111-130	172-210							
PRPB STAAL	REPLICATION INITIATION PROTEIN	STAPHYLOCOCCUS AUREUS	388-315								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	168-195	297-324	343-373						
PRPB STAAL	REPLICATION INITIATION PROTEIN	CLOSTRIDIUM PERFRINGENS	119-148	205-243							
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	119-148	205-243							
PRPB STAAL	REPLICATION INITIATION PROTEIN	LACTOBACILLUS PLANTARUM	119-148	205-243							
PRPB STAAL	REPLICATION INITIATION PROTEIN	CLOSTRIDIUM PERFRINGENS	68-102	151-185							
PRPB STAAL	REPLICATION INITIATION PROTEIN	BACILLUS SUBTILIS	34-48								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	86-113	183-204							
PRPB STAAL	REPLICATION INITIATION PROTEIN	SALMONELLA TYPHIMURIUM	86-113	183-204							
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	180-210	443-473							
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	199-228								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	185-212								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	37-66	237-268							
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	84-95	145-172	210-261						
PRPB STAAL	REPLICATION INITIATION PROTEIN	SALMONELLA TYPHIMURIUM	335-369								
PRPB STAAL	REPLICATION INITIATION PROTEIN	SALMONELLA TYPHIMURIUM	366-393								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	326-360								
PRPB STAAL	REPLICATION INITIATION PROTEIN	SALMONELLA TYPHIMURIUM	8-31								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	81-89	184-240							
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	18-45								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	3-20	85-113							
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	220-259								
PRPB STAAL	REPLICATION INITIATION PROTEIN	SALMONELLA TYPHIMURIUM	212-261								
PRPB STAAL	REPLICATION INITIATION PROTEIN	SALMONELLA TYPHIMURIUM	22-54	205-232							
PRPB STAAL	REPLICATION INITIATION PROTEIN	VIBRIO ANGUILLARUM	140-216								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	91-110								
PRPB STAAL	REPLICATION INITIATION PROTEIN	BACILLUS THURINGIENSIS	15-68	190-262	310-393						
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	175-202								
PRPB STAAL	REPLICATION INITIATION PROTEIN	SALMONELLA TYPHIMURIUM	175-202								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	10-41								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	152-179								
PRPB STAAL	REPLICATION INITIATION PROTEIN	RHIZOBIUM LEGUMINOSARUM	206-233								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	118-165								
PRPB STAAL	REPLICATION INITIATION PROTEIN	BORRELIA BURGDORFERI	215-242	327-369							
PRPB STAAL	REPLICATION INITIATION PROTEIN	BACILLUS SUBTILIS	82-109								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	667-694								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	380-414	667-694	1016-1081						
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	671-712	1071-1098							
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	345-372								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	93-127								
PRPB STAAL	REPLICATION INITIATION PROTEIN	ESCHERICHIA COLI	167-194								
PRPB STAAL	REPLICATION INITIATION PROTEIN	PHOTOBACTERIUM LEIOGNATHI	2-47	131-158							
PRPB STAAL	REPLICATION INITIATION PROTEIN	BACILLUS SUBTILIS	8-33								
PRPB STAAL	REPLICATION INITIATION PROTEIN	PHOTOBACTERIUM LEIOGNATHI	14-43								
PRPB STAAL	REPLICATION INITIATION PROTEIN	STREPTOCOCCUS ANTIDOTICUS	14-72	106-133							
PRPB STAAL	REPLICATION INITIATION PROTEIN	SYNEDIOSYSTIS SP	2-34								

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[illegible]

GENE	19711814	Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	ORGANISM	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
PSAP_BACSU	SENSOR PROTEIN SPK	BACILLUS SUBTILIS	90-107	224-351	290-374						
PSAP_STRSU	CELL SURFACE ANTIGEN VII PRECURSOR	STREPTOCOCCUS MUTANS	132-276	281-465	538-565	576-630	1071-1091	1153-1182	1371-1400		
PSAP_BACSU	REGULATORY PROTEIN	BACILLUS SUBTILIS	4-31	172-199							
PSAP_BACSU	SUBTILIN TRANSPORT PROTEIN SPAT	BACILLUS SUBTILIS	55-83	226-263							
PSFC_STRSY	EXOTOXIN TYPE C PRECURSOR	STREPTOCOCCUS PYOGENES	12-39	153-182							
PSPIR_SPTCI	SPIRALIN	SPIROPLASMA CITRI	82-109								
PSPIR_SPTCI	SPIRALIN	SPIROPLASMA MELLIFERUM	193-232								
PSPT_ECOLI	GUAN-7,5-BIS(DIPHOS) 3'-PYROPHOSPHODIHYDROLASE IV	ESCHERICHIA COLI	617-664								
PSPP_ECOLI	PROTEASE IV	ESCHERICHIA COLI	378-385								
PSQC_ZYMOBIO	SQUALENE-HOPANE CYCLASE	ZYMONOHAES MOBILIS	590-617								
PSPA_BACSU	SQUALEN SYNTHETASE SUBUNIT A	BACILLUS SUBTILIS	159-186								
PSAP_ECOLI	SIGNAL RECOGNITION PARTICLE PROTEIN	ESCHERICHIA COLI	301-328								
PSAP_MYOMY	SIGNAL RECOGNITION PARTICLE PROTEIN	MYCOPLASMA MYCOIDES	31-65	102-141	304-428						
PSAP_PASHA	SEROTYPE-SPECIFIC ANTIGEN I PRECURSOR	PASTURELLA HAEMOLYTICA	131-178	358-383	465-518	539-570	660-694				
PSAB_STRPA	ADHESIN B PRECURSOR	STREPTOCOCCUS PARASANGUIS	32-59								
PSAB_STRPA	ADHESIN B PRECURSOR	STREPTOCOCCUS SANGUIS	21-59	101-128							
PSAB_ECOLI	SINGLE-STRAND BINDING PROTEIN	ESCHERICHIA COLI	68-93								
PSBB_PONDI	SINGLE-STRAND BINDING PROTEIN	PROTEUS MIRABILIS	63-104								
PSBB_PONDI	SINGLE-STRAND BINDING PROTEIN	SERRATIA MARCESCENS	91-104								
PSBB_PONDI	SINGLE-STRAND BINDING PROTEIN	STREPTOCOCCUS SANGUIS	131-173	178-287	293-483	563-592	676-710	1081-1121			
PSAV_STRAV	AGGLUTININ RECEPTOR PRECURSOR	STREPTOCOCCUS AVIRIDII	123-132								
PSAV_STRAV	AGGLUTININ RECEPTOR PRECURSOR	ESCHERICHIA COLI	66-93								
PSIC_ECOLI	STREPTOCHITIN ACETYL TRANSFERASE	STREPTOCOCCUS AUREUS	90-119	172-199	210-311						
PSIC_STAAU	STAPHYLOCOAGULASE PRECURSOR	STAPHYLOCOCCUS AUREUS	90-117	204-291							
PSIC_STAAU	STAPHYLOCOAGULASE PRECURSOR	STAPHYLOCOCCUS AUREUS	47-74								
PSIC_CLORE	L-TRANS-TRANS-CONJUG. PROTEIN	CLOSTRIDIUM BEIJECKII	41-74								
PSIC_ECOLI	SITPA PROTEIN	ESCHERICHIA COLI	36-63								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	STREPTOCOCCUS GRISEUS	183-210								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	STREPTOCOCCUS EQUIMILIS	209-236	281-308							
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	STREPTOCOCCUS PYOGENES	209-236								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	STREPTOCOCCUS SP	209-236	281-308							
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SUBTILIS	413-462	532-563	603-639						
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SUBTILIS	40-67	88-116	121-148	534-597					
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SUBTILIS	27-74								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	STREPTOCOCCUS SP	63-94								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	STREPTOCOCCUS SP	64-91								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	STREPTOCOCCUS SP	191-222								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS LUTEMIFORMIS	91-118								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS MESENTERICUS	91-118								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SP	36-63	250-277							
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SUBTILIS	197-224								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SUBTILIS	197-224								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SUBTILIS	197-224								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SUBTILIS	55-108	613-634	741-768						
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	ESCHERICHIA COLI	63-89								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	AGROBACTERIUM VIITIS	449-476								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	ENTEROBACTER AEROGENES	112-139								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	ESCHERICHIA COLI	257-287	723-753	790-821						
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	ESCHERICHIA COLI	310-357								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	ESCHERICHIA COLI	49-76								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS STEAROTHEAOPHILUS	40-76	351-376							
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SUBTILIS	40-76								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	THEMAUS AQUATICUS	7-34								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SUBTILIS	300-367	403-441							
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	BACILLUS SUBTILIS	340-373	403-434	744-771						
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	ESCHERICHIA COLI	374-383	487-514							
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	STREPTOCOCCUS EQUIMILIS	378-403								
PSIR_STRGR	IMOSAMINE PHOSPHATE AMIDINOTRANSFERASE I	METHANOBACTERIUM THERMAUTOTROPICUM	1010-1033								

ECGENE	10717184	Prokaryotic Sequence	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10	AREA.11	AREA.12	AREA.13	AREA.14	AREA.15	AREA.16	AREA.17	AREA.18	AREA.19	AREA.20	AREA.21	AREA.22	AREA.23	AREA.24	AREA.25	AREA.26	AREA.27	AREA.28	AREA.29	AREA.30	AREA.31	AREA.32	AREA.33	AREA.34	AREA.35	AREA.36	AREA.37	AREA.38	AREA.39	AREA.40	AREA.41	AREA.42	AREA.43	AREA.44	AREA.45	AREA.46	AREA.47	AREA.48	AREA.49	AREA.50	AREA.51	AREA.52	AREA.53	AREA.54	AREA.55	AREA.56	AREA.57	AREA.58	AREA.59	AREA.60	AREA.61	AREA.62	AREA.63	AREA.64	AREA.65	AREA.66	AREA.67	AREA.68	AREA.69	AREA.70	AREA.71	AREA.72	AREA.73	AREA.74	AREA.75	AREA.76	AREA.77	AREA.78	AREA.79	AREA.80	AREA.81	AREA.82	AREA.83	AREA.84	AREA.85	AREA.86	AREA.87	AREA.88	AREA.89	AREA.90	AREA.91	AREA.92	AREA.93	AREA.94	AREA.95	AREA.96	AREA.97	AREA.98	AREA.99	AREA.100	AREA.101	AREA.102	AREA.103	AREA.104	AREA.105	AREA.106	AREA.107	AREA.108	AREA.109	AREA.110	AREA.111	AREA.112	AREA.113	AREA.114	AREA.115	AREA.116	AREA.117	AREA.118	AREA.119	AREA.120	AREA.121	AREA.122	AREA.123	AREA.124	AREA.125	AREA.126	AREA.127	AREA.128	AREA.129	AREA.130	AREA.131	AREA.132	AREA.133	AREA.134	AREA.135	AREA.136	AREA.137	AREA.138	AREA.139	AREA.140	AREA.141	AREA.142	AREA.143	AREA.144	AREA.145	AREA.146	AREA.147	AREA.148	AREA.149	AREA.150	AREA.151	AREA.152	AREA.153	AREA.154	AREA.155	AREA.156	AREA.157	AREA.158	AREA.159	AREA.160	AREA.161	AREA.162	AREA.163	AREA.164	AREA.165	AREA.166	AREA.167	AREA.168	AREA.169	AREA.170	AREA.171	AREA.172	AREA.173	AREA.174	AREA.175	AREA.176	AREA.177	AREA.178	AREA.179	AREA.180	AREA.181	AREA.182	AREA.183	AREA.184	AREA.185	AREA.186	AREA.187	AREA.188	AREA.189	AREA.190	AREA.191	AREA.192	AREA.193	AREA.194	AREA.195	AREA.196	AREA.197	AREA.198	AREA.199	AREA.200	AREA.201	AREA.202	AREA.203	AREA.204	AREA.205	AREA.206	AREA.207	AREA.208	AREA.209	AREA.210	AREA.211	AREA.212	AREA.213	AREA.214	AREA.215	AREA.216	AREA.217	AREA.218	AREA.219	AREA.220	AREA.221	AREA.222	AREA.223	AREA.224	AREA.225	AREA.226	AREA.227	AREA.228	AREA.229	AREA.230	AREA.231	AREA.232	AREA.233	AREA.234	AREA.235	AREA.236	AREA.237	AREA.238	AREA.239	AREA.240	AREA.241	AREA.242	AREA.243	AREA.244	AREA.245	AREA.246	AREA.247	AREA.248	AREA.249	AREA.250	AREA.251	AREA.252	AREA.253	AREA.254	AREA.255	AREA.256	AREA.257	AREA.258	AREA.259	AREA.260	AREA.261	AREA.262	AREA.263	AREA.264	AREA.265	AREA.266	AREA.267	AREA.268	AREA.269	AREA.270	AREA.271	AREA.272	AREA.273	AREA.274	AREA.275	AREA.276	AREA.277	AREA.278	AREA.279	AREA.280	AREA.281	AREA.282	AREA.283	AREA.284	AREA.285	AREA.286	AREA.287	AREA.288	AREA.289	AREA.290	AREA.291	AREA.292	AREA.293	AREA.294	AREA.295	AREA.296	AREA.297	AREA.298	AREA.299	AREA.300	AREA.301	AREA.302	AREA.303	AREA.304	AREA.305	AREA.306	AREA.307	AREA.308	AREA.309	AREA.310	AREA.311	AREA.312	AREA.313	AREA.314	AREA.315	AREA.316	AREA.317	AREA.318	AREA.319	AREA.320	AREA.321	AREA.322	AREA.323	AREA.324	AREA.325	AREA.326	AREA.327	AREA.328	AREA.329	AREA.330	AREA.331	AREA.332	AREA.333	AREA.334	AREA.335	AREA.336	AREA.337	AREA.338	AREA.339	AREA.340	AREA.341	AREA.342	AREA.343	AREA.344	AREA.345	AREA.346	AREA.347	AREA.348	AREA.349	AREA.350	AREA.351	AREA.352	AREA.353	AREA.354	AREA.355	AREA.356	AREA.357	AREA.358	AREA.359	AREA.360	AREA.361	AREA.362	AREA.363	AREA.364	AREA.365	AREA.366	AREA.367	AREA.368	AREA.369	AREA.370	AREA.371	AREA.372	AREA.373	AREA.374	AREA.375	AREA.376	AREA.377	AREA.378	AREA.379	AREA.380	AREA.381	AREA.382	AREA.383	AREA.384	AREA.385	AREA.386	AREA.387	AREA.388	AREA.389	AREA.390	AREA.391	AREA.392	AREA.393	AREA.394	AREA.395	AREA.396	AREA.397	AREA.398	AREA.399	AREA.400	AREA.401	AREA.402	AREA.403	AREA.404	AREA.405	AREA.406	AREA.407	AREA.408	AREA.409	AREA.410	AREA.411	AREA.412	AREA.413	AREA.414	AREA.415	AREA.416	AREA.417	AREA.418	AREA.419	AREA.420	AREA.421	AREA.422	AREA.423	AREA.424	AREA.425	AREA.426	AREA.427	AREA.428	AREA.429	AREA.430	AREA.431	AREA.432	AREA.433	AREA.434	AREA.435	AREA.436	AREA.437	AREA.438	AREA.439	AREA.440	AREA.441	AREA.442	AREA.443	AREA.444	AREA.445	AREA.446	AREA.447	AREA.448	AREA.449	AREA.450	AREA.451	AREA.452	AREA.453	AREA.454	AREA.455	AREA.456	AREA.457	AREA.458	AREA.459	AREA.460	AREA.461	AREA.462	AREA.463	AREA.464	AREA.465	AREA.466	AREA.467	AREA.468	AREA.469	AREA.470	AREA.471	AREA.472	AREA.473	AREA.474	AREA.475	AREA.476	AREA.477	AREA.478	AREA.479	AREA.480	AREA.481	AREA.482	AREA.483	AREA.484	AREA.485	AREA.486	AREA.487	AREA.488	AREA.489	AREA.490	AREA.491	AREA.492	AREA.493	AREA.494	AREA.495	AREA.496	AREA.497	AREA.498	AREA.499	AREA.500	AREA.501	AREA.502	AREA.503	AREA.504	AREA.505	AREA.506	AREA.507	AREA.508	AREA.509	AREA.510	AREA.511	AREA.512	AREA.513	AREA.514	AREA.515	AREA.516	AREA.517	AREA.518	AREA.519	AREA.520	AREA.521	AREA.522	AREA.523	AREA.524	AREA.525	AREA.526	AREA.527	AREA.528	AREA.529	AREA.530	AREA.531	AREA.532	AREA.533	AREA.534	AREA.535	AREA.536	AREA.537	AREA.538	AREA.539	AREA.540	AREA.541	AREA.542	AREA.543	AREA.544	AREA.545	AREA.546	AREA.547	AREA.548	AREA.549	AREA.550	AREA.551	AREA.552	AREA.553	AREA.554	AREA.555	AREA.556	AREA.557	AREA.558	AREA.559	AREA.560	AREA.561	AREA.562	AREA.563	AREA.564	AREA.565	AREA.566	AREA.567	AREA.568	AREA.569	AREA.570	AREA.571	AREA.572	AREA.573	AREA.574	AREA.575	AREA.576	AREA.577	AREA.578	AREA.579	AREA.580	AREA.581	AREA.582	AREA.583	AREA.584	AREA.585	AREA.586	AREA.587	AREA.588	AREA.589	AREA.590	AREA.591	AREA.592	AREA.593	AREA.594	AREA.595	AREA.596	AREA.597	AREA.598	AREA.599	AREA.600	AREA.601	AREA.602	AREA.603	AREA.604	AREA.605	AREA.606	AREA.607	AREA.608	AREA.609	AREA.610	AREA.611	AREA.612	AREA.613	AREA.614	AREA.615	AREA.616	AREA.617	AREA.618	AREA.619	AREA.620	AREA.621	AREA.622	AREA.623	AREA.624	AREA.625	AREA.626	AREA.627	AREA.628	AREA.629	AREA.630	AREA.631	AREA.632	AREA.633	AREA.634	AREA.635	AREA.636	AREA.637	AREA.638	AREA.639	AREA.640	AREA.641	AREA.642	AREA.643	AREA.644	AREA.645	AREA.646	AREA.647	AREA.648	AREA.649	AREA.650	AREA.651	AREA.652	AREA.653	AREA.654	AREA.655	AREA.656	AREA.657	AREA.658	AREA.659	AREA.660	AREA.661	AREA.662	AREA.663	AREA.664	AREA.665	AREA.666	AREA.667	AREA.668	AREA.669	AREA.670	AREA.671	AREA.672	AREA.673	AREA.674	AREA.675	AREA.676	AREA.677	AREA.678	AREA.679	AREA.680	AREA.681	AREA.682	AREA.683	AREA.684	AREA.685	AREA.686	AREA.687	AREA.688	AREA.689	AREA.690	AREA.691	AREA.692	AREA.693	AREA.694	AREA.695	AREA.696	AREA.697	AREA.698	AREA.699	AREA.700	AREA.701	AREA.702	AREA.703	AREA.704	AREA.705	AREA.706	AREA.707	AREA.708	AREA.709	AREA.710	AREA.711	AREA.712	AREA.713	AREA.714	AREA.715	AREA.716	AREA.717	AREA.718	AREA.719	AREA.720	AREA.721	AREA.722	AREA.723	AREA.724	AREA.725	AREA.726	AREA.727	AREA.728	AREA.729	AREA.730	AREA.731	AREA.732	AREA.733	AREA.734	AREA.735	AREA.736	AREA.737	AREA.738	AREA.739	AREA.740	AREA.741	AREA.742	AREA.743	AREA.744	AREA.745	AREA.746	AREA.747	AREA.748	AREA.749	AREA.750	AREA.751	AREA.752	AREA.753	AREA.754	AREA.755	AREA.756	AREA.757	AREA.758	AREA.759	AREA.760	AREA.761	AREA.762	AREA.763	AREA.764	AREA.765	AREA.766	AREA.767	AREA.768	AREA.769	AREA.770	AREA.771	AREA.772	AREA.773	AREA.774	AREA.775	AREA.776	AREA.777	AREA.778	AREA.779	AREA.780	AREA.781	AREA.782	AREA.783	AREA.784	AREA.785	AREA.786	AREA.787	AREA.788	AREA.789	AREA.790	AREA.791	AREA.792	AREA.793	AREA.794	AREA.795	AREA.796	AREA.797	AREA.798	AREA.799	AREA.800	AREA.801	AREA.802	AREA.803	AREA.804	AREA.805	AREA.806	AREA.807	AREA.808	AREA.809	AREA.810	AREA.811	AREA.812	AREA.813	AREA.814	AREA.815	AREA.816	AREA.817	AREA.818	AREA.819	AREA.820	AREA.821	AREA.822	AREA.823	AREA.824	AREA.825	AREA.826	AREA.827	AREA.828	AREA.829	AREA.830	AREA.831	AREA.832	AREA.833	AREA.834	AREA.835	AREA.836	AREA.837	AREA.838	AREA.839	AREA.840	AREA.841	AREA.842	AREA.843	AREA.844	AREA.845	AREA.846	AREA.847	AREA.848	AREA.849	AREA.850	AREA.851	AREA.852	AREA.853	AREA.854	AREA.855	AREA.856	AREA.857	AREA.858	AREA.859	AREA.860	AREA.861	AREA.862	AREA.863	AREA.864	AREA.865	AREA.866	AREA.867	AREA.868	AREA.869	AREA.870	AREA.871	AREA.872	AREA.873	AREA.874	AREA.875	AREA.876	AREA.877	AREA.878	AREA.879	AREA.880	AREA.881	AREA.882	AREA.883	AREA.884	AREA.885	AREA.886	AREA.887	AREA.888	AREA.889	AREA.890	AREA.891	AREA.892	AREA.893	AREA.894	AREA.895	AREA.896	AREA.897	AREA.898	AREA.899	AREA.900	AREA.901	AREA.902	AREA.903	AREA.904	AREA.905	AREA.906	AREA.907	AREA.908	AREA.909	AREA.910	AREA.911	AREA.912	AREA.913	AREA.914	AREA.915	AREA.916	AREA.917	AREA.918	AREA.919	AREA.920	AREA.921	AREA.922	AREA.923	AREA.924	AREA.925	AREA.926	AREA.927	AREA.928	AREA.929	AREA.930	AREA.931	AREA.932	AREA.933	AREA.934	AREA.935	AREA.936	AREA.937	AREA.938	AREA.939	AREA.940	AREA.941	AREA.942	AREA.943	AREA.944	AREA.945	AREA.946	AREA.947	AREA.948	AREA.949	AREA.950	AREA.951	AREA.952	AREA.953	AREA.954	AREA.955	AREA.956	AREA.957	AREA.958	AREA.959	AREA.960	AREA.961	AREA.962	AREA.963	AREA.964	AREA.965	AREA.966	AREA.967	AREA.968	AREA.969	AREA.970	AREA.971	AREA.972	AREA.973	AREA.974	AREA.975	AREA.976	AREA.977	AREA.978	AREA.979	AREA.980	AREA.981	AREA.982	AREA.983	AREA.984	AREA.985	AREA.986	AREA.987	AREA.988	AREA.989	AREA.990	AREA.991	AREA.992	AREA.993	AREA.994	AREA.995	AREA.996	AREA.997	AREA.998	AREA.999	AREA.1000
ECGENE	10717184	Prokaryotic Sequence	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8	AREA.9	AREA.10	AREA.11	AREA.12	AREA.13	AREA.14	AREA.15	AREA.16	AREA.17	AREA.18	AREA.19	AREA.20	AREA.21	AREA.22	AREA.23	AREA.24	AREA.25	AREA.26	AREA.27	AREA.28	AREA.29	AREA.30	AREA.31	AREA.32	AREA.33	AREA.34	AREA.35	AREA.36	AREA.37	AREA.38	AREA.39	AREA.40	AREA.41	AREA.42	AREA.43	AREA.44	AREA.45	AREA.46	AREA.47	AREA.48	AREA.49	AREA.50	AREA.51	AREA.52	AREA.53	AREA.54	AREA.55	AREA.56	AREA.57	AREA.58	AREA.59	AREA.60	AREA.61	AREA.62	AREA.63	AREA.64	AREA.65	AREA.66	AREA.67	AREA.68	AREA.69	AREA.70	AREA.71	AREA.72	AREA.73	AREA.74	AREA.75	AREA.76	AREA.77	AREA.78	AREA.79	AREA.80	AREA.81	AREA.82	AREA.83	AREA.84	AREA.85	AREA.86	AREA.87	AREA.88	AREA.89	AREA.90	AREA.91	AREA.92	AREA.93	AREA.94	AREA.95	AREA.96	AREA.97	AREA.98	AREA.99	AREA.100	AREA.101	AREA.102	AREA.103	AREA.104	AREA.105	AREA.106	AREA.107	AREA.108	AREA.109	AREA.110	AREA.111	AREA.112	AREA.113	AREA.114	AREA.115	AREA.116	AREA.117	AREA.118	AREA.119	AREA.120	AREA.121	AREA.122	AREA.123	AREA.124	AREA.125	AREA.126	AREA.127	AREA.128	AREA.129	AREA.130	AREA.131	AREA.132	AREA.133	AREA.134	AREA.135	AREA.136	AREA.137	AREA.138	AREA.139	AREA.140	AREA.141	AREA.142	AREA.143	AREA.144	AREA.145	AREA.146	AREA.147	AREA.148	AREA.149	AREA.150	AREA.151	AREA.152	AREA.153	AREA.154	AREA.155	AREA.156	AREA.157	AREA.158	AREA.159	AREA.160	AREA.161	AREA.162	AREA.163	AREA.164	AREA.165	AREA.166	AREA.167	AREA.168	AREA.169	AREA.170	AREA.171	AREA.172	AREA.173	AREA.174	AREA.175	AREA.176	AREA.177	AREA.178	AREA.179	AREA.180	AREA.181	AREA.182	AREA.183	AREA.184	AREA.185	AREA.186	AREA.187	AREA.188	AREA.189	AREA.190	AREA.191	AREA.192	AREA.193	AREA.194	AREA.195	AREA.196	AREA.197	AREA.198	AREA.199	AREA.200	AREA.201	AREA.202	AREA.203	AREA.204	AREA.205	AREA.206	AREA.207	AREA.208	AREA.209	AREA.210	AREA.211	AREA.212	AREA.213	AREA.214	AREA.215	AREA.216	AREA.217	AREA.218	AREA.219	AREA.220	AREA.221	AREA.222	AREA.223	AREA.224	AREA.225	AREA.226	AREA.227	AREA.228	AREA.229	AREA.230	AREA.231	AREA.232	AREA.233	AREA.234	AREA.235	AREA.236	AREA.237	AREA.238	AREA.239	AREA.240	AREA.241	AREA.242	AREA.243	AREA.244	AREA.245	AREA.246	AREA.247	AREA.248	AREA.249	AREA.250	AREA.251	AREA.252	AREA.253																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											

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PCGENE	FILE NAME	PROTEIN	FUNCTION	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 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896	AREA 897	AREA 898	AREA 899	AREA 900	AREA 901	AREA 902	AREA 903	AREA 904	AREA 905	AREA 906	AREA 907	AREA 908	AREA 909	AREA 910	AREA 911	AREA 912	AREA 913	AREA 914	AREA 915	AREA 916	AREA 917	AREA 918	AREA 919	AREA 920	AREA 921	AREA 922	AREA 923	AREA 924	AREA 925	AREA 926	AREA 927	AREA 928	AREA 929	AREA 930	AREA 931	AREA 932	AREA 933	AREA 934	AREA 935	AREA 936	AREA 937	AREA 938	AREA 939	AREA 940	AREA 941	AREA 942	AREA 943	AREA 944	AREA 945	AREA 946	AREA 947	AREA 948	AREA 949	AREA 950	AREA 951	AREA 952	AREA 953	AREA 954	AREA 955	AREA 956	AREA 957	AREA 958	AREA 959	AREA 960	AREA 961	AREA 962	AREA 963	AREA 964	AREA 965	AREA 966	AREA 967	AREA 968	AREA 969	AREA 970	AREA 971	AREA 972	AREA 973	AREA 974	AREA 975	AREA 976	AREA 977	AREA 978	AREA 979	AREA 980	AREA 981	AREA 982	AREA 983	AREA 984	AREA 985	AREA 986	AREA 987	AREA 988	AREA 989	AREA 990	AREA 991	AREA 992	AREA 993	AREA 994	AREA 995	AREA 996	AREA 997	AREA 998	AREA 999	AREA 1000
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Sequences		AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
PGCENE	10/11/18/4	Prokaryotic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	

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Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
PROJIN		AGROBACTERIUM TUMEFACIENS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										</																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														

PCGENE	1011114	Proteolytic Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILE NAME	PROTEIN	ORGANISM	244-271	272-300						
PTD5_BACSU	HYPOTHETICAL 316 KD PROTEIN	BACILLUS SUBTILIS								
PTD5_LEPBI	HYPOTHETICAL 31 KD PROTEIN	LEPTOSPIRA BIFLEXA	94-117							
PTD5_LACLA	HYPOTHETICAL 193 KD PROTEIN	LACTOCOCCUS LACTIS	76-112							
PTD5_BACSU	HYPOTHETICAL 19 KD PROTEIN	BACILLUS SUBTILIS	17-64							
PTD5_SPICI	HYPOTHETICAL 218 KD PROTEIN	SPIROPLASMA CITRI	102-149							
PTD5_BACSU	HYPOTHETICAL 118 KD PROTEIN	BACILLUS SUBTILIS	17-64	89-91						
PTD5_BACSU	HYPOTHETICAL 210 KD PROTEIN	BACILLUS SUBTILIS	142-169							
PTD5_BACSU	HYPOTHETICAL 269 KD PROTEIN	BACILLUS SUBTILIS	17-31							
PTD5_BACSU	HYPOTHETICAL 618 KD PROTEIN	BACILLUS SUBTILIS	163-207	202-289						
PTD5_BACSU	HYPOTHETICAL 648 KD PROTEIN	BACILLUS SUBTILIS	3-30	34-41	94-143					
PTD5_BACSU	HYPOTHETICAL 311 KD PROTEIN	BACILLUS SUBTILIS	36-83	85-112						
PTD5_BACSU	HYPOTHETICAL 313 KD PROTEIN	BACILLUS SUBTILIS	24-38							
PTD5_ANASP	HYPOTHETICAL 189 KD PROTEIN	ANABAEANA SP	77-104							
PTD5_CALSA	HYPOTHETICAL 107 KD PROTEIN	CALDOCELLUM SACCHAROLYTICUM	6-19							
PTD5_CALSA	HYPOTHETICAL PROTEIN	CALDOCELLUM SACCHAROLYTICUM	41-84							
PTD5_ECOLI	HYPOTHETICAL 167 KD PROTEIN	ESCHERICHIA COLI	41-78							

TABLE IX

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS

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PCGENE	FILE NAME	1011184 Mail Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000	AREA1001	AREA1002	AREA1003	AREA1004	AREA1005	AREA1006	AREA1007	AREA1008	AREA1009	AREA1010	AREA1011	AREA1012	AREA1013	AREA1014	AREA1015	AREA1016	AREA1017	AREA1018	AREA1019	AREA1020	AREA1021	AREA1022	AREA1023	AREA1024	AREA1025	AREA1026	AREA1027	AREA1028	AREA1029	AREA1030	AREA1031	AREA1032	AREA1033	AREA1034	AREA1035	AREA1036	AREA1037	AREA1038	AREA1039	AREA1040	AREA1041	AREA1042	AREA1043	AREA1044	AREA1045	AREA1046	AREA1047	AREA1048	AREA1049	AREA1050	AREA1051	AREA1052	AREA1053	AREA1054	AREA1055	AREA1056	AREA1057	AREA1058	AREA1059	AREA1060	AREA1061	AREA1062	AREA1063	AREA1064	AREA1065	AREA1066	AREA1067	AREA1068	AREA1069	AREA1070	AREA1071	AREA1072	AREA1073	AREA1074	AREA1075	AREA1076	AREA1077	AREA1078	AREA1079	AREA1080	AREA1081	AREA1082	AREA1083	AREA1084	AREA1085	AREA1086	AREA1087	AREA1088	AREA1089	AREA1090	AREA1091	AREA1092	AREA1093	AREA1094	AREA1095	AREA1096	AREA1097	AREA1098	AREA1099	AREA1100	AREA1101	AREA1102	AREA1103	AREA1104	AREA1105	AREA1106	AREA1107	AREA1108	AREA1109	AREA1110	AREA1111	AREA1112	AREA1113	AREA1114	AREA1115	AREA1116	AREA1117	AREA1118	AREA1119	AREA1120	AREA1121	AREA1122	AREA1123	AREA1124	AREA1125	AREA1126	AREA1127	AREA1128	AREA1129	AREA1130	AREA1131	AREA1132	AREA1133	AREA1134	AREA1135	AREA1136	AREA1137	AREA1138	AREA1139	AREA1140	AREA1141	AREA1142	AREA1143	AREA1144	AREA1145	AREA1146	AREA1147	AREA1148	AREA1149	AREA1150	AREA1151	AREA1152	AREA1153	AREA1154	AREA1155	AREA1156	AREA1157	AREA1158	AREA1159	AREA1160	AREA1161	AREA1162	AREA1163	AREA1164	AREA1165	AREA1166	AREA1167	AREA1168	AREA1169	AREA1170	AREA1171	AREA1172	AREA1173	AREA1174	AREA1175	AREA1176	AREA1177	AREA1178	AREA1179	AREA1180	AREA1181	AREA1182	AREA1183	AREA1184	AREA1185	AREA1186	AREA1187	AREA1188	AREA1189	AREA1190	AREA1191	AREA1192	AREA1193	AREA1194	AREA1195	AREA1196	AREA1197	AREA1198	AREA1199	AREA1200	AREA1201	AREA1202	AREA1203	AREA1204	AREA1205	AREA1206	AREA1207	AREA1208	AREA1209	AREA1210	AREA1211	AREA1212	AREA1213	AREA1214	AREA1215	AREA1216	AREA1217	AREA1218	AREA1219	AREA1220	AREA1221	AREA1222	AREA1223	AREA1224	AREA1225	AREA1226	AREA1227	AREA1228	AREA1229	AREA1230	AREA1231	AREA1232	AREA1233	AREA1234	AREA1235	AREA1236	AREA1237	AREA1238	AREA1239	AREA1240	AREA1241	AREA1242	AREA1243	AREA1244	AREA1245	AREA1246	AREA1247	AREA1248	AREA1249	AREA1250	AREA1251	AREA1252	AREA1253	AREA1254	AREA1255	AREA1256	AREA1257	AREA1258	AREA1259	AREA1260	AREA1261	AREA1262	AREA1263	AREA1264	AREA1265	AREA1266	AREA1267	AREA1268	AREA1269	AREA1270	AREA1271	AREA1272	AREA1273	AREA1274	AREA1275	AREA1276	AREA1277	AREA1278	AREA1279	AREA1280	AREA1281	AREA1282	AREA1283	AREA1284	AREA1285	AREA1286	AREA1287	AREA1288	AREA1289	AREA1290	AREA1291	AREA1292	AREA1293	AREA1294	AREA1295	AREA1296	AREA1297	AREA1298	AREA1299	AREA1300	AREA1301	AREA1302	AREA1303	AREA1304	AREA1305	AREA1306	AREA1307	AREA1308	AREA1309	AREA1310	AREA1311	AREA1312	AREA1313	AREA1314	AREA1315	AREA1316	AREA1317	AREA1318	AREA1319	AREA1320	AREA1321	AREA1322	AREA1323	AREA1324	AREA1325	AREA1326	AREA1327	AREA1328	AREA1329	AREA1330	AREA1331	AREA1332	AREA1333	AREA1334	AREA1335	AREA1336	AREA1337	AREA1338	AREA1339	AREA1340	AREA1341	AREA1342	AREA1343	AREA1344	AREA1345	
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PCGENE	1021784a Methyl Search on All Human Protein Sequences	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
FILE NAME	PROTEIN	AREA.1	AREA.2	AREA.3	AREA.4	AREA.5	AREA.6	AREA.7	AREA.8
PF001 HUMAN	EXCISION REPAIR PROTEIN ERCC-4	160-200							
PF002 HUMAN	ESTROGEN RECEPTOR (ER)	451-488							
PF003 HUMAN	ENDOTHELIN-1 PRECURSOR (ET-1)	131-160							
PF004 HUMAN	ENDOTHELIN-3 PRECURSOR (ET-3)	182-209							
PF005 HUMAN	EVIA PROTEIN PRECURSOR	38-56							
PF006 HUMAN	ETA1 (P11) (OTYVOLLIN) (VILLIN-1)	119-146	331-392	402-429	512-519				
PF007 HUMAN	COAGULATION FACTOR V PRECURSOR	2103-2137							
PF008 HUMAN	COAGULATION FACTOR VIII PRECURSOR (PROCOAGULANT COMPONENT)	871-908	1007-1034	1194-1210					
PF009 HUMAN	COAGULATION FACTOR IX PRECURSOR (EC 2.1.2.1) (CHRISTMAS FACTOR)	271-298							
PF010 HUMAN	FATTY ACID-BINDING PROTEIN, INTESTINAL	98-125							
PF011 HUMAN	APOLYFOS-ACIDATING SURFACE ANTIGEN FAS PRECURSOR (APO-1 ANTIGEN)	23-50	249-301	308-333					
PF012 HUMAN	LOW AFFINITY DANTHROGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE)	81-115							
PF013 HUMAN	HIGH AFFINITY DANTHROGLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT (FCER1)	140-174							
PF014 HUMAN	FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (EC 2.1.1.13)	310-337							
PF015 HUMAN	FIBRINOGEN ALPHA CHAIN PRECURSOR	131-165	427-457						
PF016 HUMAN	FIBRINOGEN BETA CHAIN PRECURSOR	149-186							
PF017 HUMAN	FIBRINOGEN GAMMA-A CHAIN PRECURSOR	59-93	173-160						
PF018 HUMAN	FIBRINOGEN GAMMA-B CHAIN (FIBRINOGEN GAMMA)	59-93	173-160						
PF019 HUMAN	FIBRINOGENIN PRECURSOR	2108-2199							
PF020 HUMAN	FL-1 ONCOGENE (BCL2 TRANSCRIPTION FACTOR)	172-209							
PF021 HUMAN	DIAGETYL ANILINE MONOOXYGENASE (N-OXIDE FORMING) 2 (EC 1.14.13.8)	184-218	236-283	301-328					
PF022 HUMAN	P53-C-FOS PROTO-ONCOGENE PROTEIN	162-193							
PF023 HUMAN	FOS-RELATED ANTIGEN 1	133-168							
PF024 HUMAN	FOS-RELATED ANTIGEN 2	149-180							
PF025 HUMAN	FERRITIN LIGHT CHAIN	2-34							
PF026 HUMAN	FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R)	3-33							
PF027 HUMAN	TISSUE ALPHA-L-FUCOSIDASE PRECURSOR (EC 2.1.1.1) (ALPHA-L-FUCOSIDASE)	364-393							
PF028 HUMAN	FUMARATE HYDRAATASE, MITOCHONDRIAL (EC 2.1.1.2) (FUMARATE)	308-335							
PF029 HUMAN	MUTATIVE LYMPHOCYTE GAGI SWITCH PROTEIN	424-451							
PF030 HUMAN	PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, HEAVY CHAIN (PKC-SH)	36-83							
PF031 HUMAN	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 2.1.1.9) (PHOSPHOGLUCOSE)	146-173							
PF032 HUMAN	MAJOR GASTROINTESTINAL TUMOR-ASSOCIATED PROTEIN GA311-2 PRECURSOR	16-50							
PF033 HUMAN	GALLACTONASE 2 (EC 2.1.1.4)	181-315							
PF034 HUMAN	GAD65-AMINO BUTYRIC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABA(A)	354-381							
PF035 HUMAN	GAD65-AMINO BUTYRIC-ACID RECEPTOR ALPHA-3 SUBUNIT PRECURSOR (GABA(A)	210-337							
PF036 HUMAN	GASTROINTESTINAL TUMOR-ASSOCIATED PROTEIN GA311-1 PRECURSOR	311-355							
PF037 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) ALPHA SUBUNIT 1	31-165							
PF038 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) ALPHA SUBUNIT 2	22-49							
PF039 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) ALPHA SUBUNIT 3	22-49							
PF040 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) ALPHA SUBUNIT (ALPHA-1)	22-49							
PF041 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) ALPHA SUBUNIT (ADENYLATE)	7-34							
PF042 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) ALPHA SUBUNIT (ALPHA-11)	91-122							
PF043 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) BETA SUBUNIT 1	61-92							
PF044 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3	110-137	235-287	289-316					
PF045 HUMAN	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 2 (GUANINE NUCLEOTIDE)	454-488							
PF046 HUMAN	GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) ALPHA-2 SUBUNIT (TRANSDUCIN)	22-49							
PF047 HUMAN	GC-RICH SEQUENCE DNA-BINDING FACTOR (GC-F) (TRANSCRIPTION FACTOR 9)	206-237	291-320	367-394	396-421	647-676			
PF048 HUMAN	GTP CYCLOHYDROLASE I (EC 2.1.4.18)	165-192							
PF049 HUMAN	GLUCOCORTICOID RECEPTOR ALPHA (GR)	167-194							
PF050 HUMAN	GLUCOCORTICOID RECEPTOR BETA (GB)	167-194							
PF051 HUMAN	GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2)	460-487							
PF052 HUMAN	GLA DEUTERON (GDM) (PROTEINASE NEKIN II)	81-110							
PF053 HUMAN	GELATIN PRECURSOR, PLASMA (ACTIN-DENATURING FACTOR) (ADF)	701-728							
PF054 HUMAN	GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE	189-216	340-376	384-411					
PF055 HUMAN	N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (GAS)	176-221							
PF056 HUMAN	GLYCEROL KINASE (EC 2.1.1.30) (ATP GLYCEROL 3-PHOSPHOTRANSFERASE)	78-112	231-278						
PF057 HUMAN	SEBINE HYDROXYMETHYLTRANSFERASE, CYTOSOLIC (EC 2.1.2.1) (SERINE)	32-59	344-371						

PGCONE	1071114c Medil Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8
FILENAME	PROTHIN	417-444							
POLY7 HUMAN	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL (EC 2.3.1.1) (SERINE)								
POR78 HUMAN	18 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78) (HSP70) (HSP70) (HSP70)	598-633							
POR83 HUMAN	GLYCINE RECEPTOR ALPHA-2 CHAIN PRECURSOR	162-169							
POR84 HUMAN	GRAVIN (FRAGMENT)	9-43							
POR85 HUMAN	GROWTH HORMONE-RELEASING HORMONE RECEPTOR PRECURSOR (GHRH RECEPTOR)	118-155							
POR86 HUMAN	GLUTATHIONE S-TRANSFERASE MA SUBUNIT 2 (EC 2.3.1.18) (GTHS2) (CLASS-)	64-91							
POT87 HUMAN	GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21) PROTEIN ACTIVATOR	414-501							
POT88 HUMAN	GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN	274-301							
POT89 HUMAN	GLUCOSE TRANSPORTER TYPE 1, BRAIN	274-301							
POT90 HUMAN	GLUCOSE TRANSPORTER TYPE 4, INSULIN-RESPONSIVE	280-317							
POT91 HUMAN	HISTONE H1	44-89							
POT92 HUMAN	HISTONE H1A (H1.1)	71-104							
POT93 HUMAN	HISTONE H1B (H1.4)	70-101							
POT94 HUMAN	HISTONE H1C (H1.3)	71-102							
POT95 HUMAN	HISTONE H1D (H1.2)	70-101							
POT96 HUMAN	HISTONE H1E (H1.1)	74-105							
POT97 HUMAN	HISTONE H2B.1	20-47							
POT98 HUMAN	HISTONE H2B.2	20-47							
POT99 HUMAN	HISTONE H2B (H2B.1 A)	20-47							
POT100 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN (DQ) ALPHA CHAIN PRECURSOR	142-169							
POT101 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN (DQ) BETA CHAIN PRECURSOR	50-83							
POT102 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN (DQ) BETA CHAIN PRECURSOR	50-77							
POT103 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN (DQ) BETA CHAIN PRECURSOR	50-77							
POT104 HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN (DQ) BETA CHAIN PRECURSOR	50-77							
POT105 HUMAN	HEPARIN-BINDING GROWTH FACTOR PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST)	102-129							
POT106 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT107 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT108 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT109 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT110 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT111 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT112 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT113 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT114 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT115 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
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POT117 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
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POT121 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
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POT123 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT124 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
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POT127 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
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POT129 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
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POT131 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
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POT135 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
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POT182 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT183 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT184 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT185 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT186 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT187 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT188 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT189 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT190 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT191 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT192 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT193 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT194 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT195 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT196 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT197 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT198 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT199 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT200 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT201 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT202 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT203 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT204 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT205 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT206 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT207 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT208 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT209 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT210 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT211 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT212 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT213 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT214 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT215 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT216 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT217 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT218 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT219 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT220 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT221 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT222 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT223 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT224 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT225 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT226 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT227 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT228 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT229 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT230 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT231 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT232 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT233 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT234 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT235 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT236 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT237 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT238 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT239 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT240 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT241 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT242 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT243 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT244 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)	61-91							
POT245 HUMAN	HBGF-1 (ACIDIC FIBROBLAST)								

10/11/13 (Mell) Search on All Human Protein Sequences									
GENE	PROTEIN	DESCRIPTION	AMPA1	AMPA2	AMPA3	AMPA4	AMPA5	AMPA6	AMPA7
IL13RA1	IL13RA1	IL-13 RECEPTOR, TYPE I (P10)	437-487						437-487
IL13RA2	IL13RA2	IL-13 RECEPTOR, TYPE II (P10)	159-186						159-186
IL13RA3	IL13RA3	IL-13 RECEPTOR, TYPE III (P10)	87-114						87-114
IL13RA4	IL13RA4	IL-13 RECEPTOR, TYPE IV (P10)	112-139						112-139
IL13RA5	IL13RA5	IL-13 RECEPTOR, TYPE V (P10)	94-121						94-121
IL13RA6	IL13RA6	IL-13 RECEPTOR, TYPE VI (P10)	90-117	300-327		300-327			300-327
IL13RA7	IL13RA7	IL-13 RECEPTOR, TYPE VII (P10)	81-129						81-129
IL13RA8	IL13RA8	IL-13 RECEPTOR, TYPE VIII (P10)	81-129						81-129
IL13RA9	IL13RA9	IL-13 RECEPTOR, TYPE IX (P10)	81-129						81-129
IL13RA10	IL13RA10	IL-13 RECEPTOR, TYPE X (P10)	81-129						81-129
IL13RA11	IL13RA11	IL-13 RECEPTOR, TYPE XI (P10)	81-129						81-129
IL13RA12	IL13RA12	IL-13 RECEPTOR, TYPE XII (P10)	81-129						81-129
IL13RA13	IL13RA13	IL-13 RECEPTOR, TYPE XIII (P10)	81-129						81-129
IL13RA14	IL13RA14	IL-13 RECEPTOR, TYPE XIV (P10)	81-129						81-129
IL13RA15	IL13RA15	IL-13 RECEPTOR, TYPE XV (P10)	81-129						81-129
IL13RA16	IL13RA16	IL-13 RECEPTOR, TYPE XVI (P10)	81-129						81-129
IL13RA17	IL13RA17	IL-13 RECEPTOR, TYPE XVII (P10)	81-129						81-129
IL13RA18	IL13RA18	IL-13 RECEPTOR, TYPE XVIII (P10)	81-129						81-129
IL13RA19	IL13RA19	IL-13 RECEPTOR, TYPE XIX (P10)	81-129						81-129
IL13RA20	IL13RA20	IL-13 RECEPTOR, TYPE XX (P10)	81-129						81-129
IL13RA21	IL13RA21	IL-13 RECEPTOR, TYPE XXI (P10)	81-129						81-129
IL13RA22	IL13RA22	IL-13 RECEPTOR, TYPE XXII (P10)	81-129						81-129
IL13RA23	IL13RA23	IL-13 RECEPTOR, TYPE XXIII (P10)	81-129						81-129
IL13RA24	IL13RA24	IL-13 RECEPTOR, TYPE XXIV (P10)	81-129						81-129
IL13RA25	IL13RA25	IL-13 RECEPTOR, TYPE XXV (P10)	81-129						81-129
IL13RA26	IL13RA26	IL-13 RECEPTOR, TYPE XXVI (P10)	81-129						81-129
IL13RA27	IL13RA27	IL-13 RECEPTOR, TYPE XXVII (P10)	81-129						81-129
IL13RA28	IL13RA28	IL-13 RECEPTOR, TYPE XXVIII (P10)	81-129						81-129
IL13RA29	IL13RA29	IL-13 RECEPTOR, TYPE XXIX (P10)	81-129						81-129
IL13RA30	IL13RA30	IL-13 RECEPTOR, TYPE XXX (P10)	81-129						81-129
IL13RA31	IL13RA31	IL-13 RECEPTOR, TYPE XXXI (P10)	81-129						81-129
IL13RA32	IL13RA32	IL-13 RECEPTOR, TYPE XXXII (P10)	81-129						81-129
IL13RA33	IL13RA33	IL-13 RECEPTOR, TYPE XXXIII (P10)	81-129						81-129
IL13RA34	IL13RA34	IL-13 RECEPTOR, TYPE XXXIV (P10)	81-129						81-129
IL13RA35	IL13RA35	IL-13 RECEPTOR, TYPE XXXV (P10)	81-129						81-129
IL13RA36	IL13RA36	IL-13 RECEPTOR, TYPE XXXVI (P10)	81-129						81-129
IL13RA37	IL13RA37	IL-13 RECEPTOR, TYPE XXXVII (P10)	81-129						81-129
IL13RA38	IL13RA38	IL-13 RECEPTOR, TYPE XXXVIII (P10)	81-129						81-129
IL13RA39	IL13RA39	IL-13 RECEPTOR, TYPE XXXIX (P10)	81-129						81-129
IL13RA40	IL13RA40	IL-13 RECEPTOR, TYPE XXXX (P10)	81-129						81-129
IL13RA41	IL13RA41	IL-13 RECEPTOR, TYPE XXXXI (P10)	81-129						81-129
IL13RA42	IL13RA42	IL-13 RECEPTOR, TYPE XXXXII (P10)	81-129						81-129
IL13RA43	IL13RA43	IL-13 RECEPTOR, TYPE XXXXIII (P10)	81-129						81-129
IL13RA44	IL13RA44	IL-13 RECEPTOR, TYPE XXXXIV (P10)	81-129						81-129
IL13RA45	IL13RA45	IL-13 RECEPTOR, TYPE XXXXV (P10)	81-129						81-129
IL13RA46	IL13RA46	IL-13 RECEPTOR, TYPE XXXXVI (P10)	81-129						81-129
IL13RA47	IL13RA47	IL-13 RECEPTOR, TYPE XXXXVII (P10)	81-129						81-129
IL13RA48	IL13RA48	IL-13 RECEPTOR, TYPE XXXXVIII (P10)	81-129						81-129
IL13RA49	IL13RA49	IL-13 RECEPTOR, TYPE XXXXIX (P10)	81-129						81-129
IL13RA50	IL13RA50	IL-13 RECEPTOR, TYPE XXXXX (P10)	81-129						81-129
IL13RA51	IL13RA51	IL-13 RECEPTOR, TYPE XXXXXI (P10)	81-129						81-129
IL13RA52	IL13RA52	IL-13 RECEPTOR, TYPE XXXXXII (P10)	81-129						81-129
IL13RA53	IL13RA53	IL-13 RECEPTOR, TYPE XXXXXIII (P10)	81-129						81-129
IL13RA54	IL13RA54	IL-13 RECEPTOR, TYPE XXXXXIV (P10)	81-129						81-129
IL13RA55	IL13RA55	IL-13 RECEPTOR, TYPE XXXXXV (P10)	81-129						81-129
IL13RA56	IL13RA56	IL-13 RECEPTOR, TYPE XXXXXVI (P10)	81-129						81-129
IL13RA57	IL13RA57	IL-13 RECEPTOR, TYPE XXXXXVII (P10)	81-129						81-129
IL13RA58	IL13RA58	IL-13 RECEPTOR, TYPE XXXXXVIII (P10)	81-129						81-129
IL13RA59	IL13RA59	IL-13 RECEPTOR, TYPE XXXXXIX (P10)	81-129						81-129
IL13RA60	IL13RA60	IL-13 RECEPTOR, TYPE XXXXXX (P10)	81-129						81-129
IL13RA61	IL13RA61	IL-13 RECEPTOR, TYPE XXXXXI (P10)	81-129						81-129
IL13RA62	IL13RA62	IL-13 RECEPTOR, TYPE XXXXXII (P10)	81-129						81-129
IL13RA63	IL13RA63	IL-13 RECEPTOR, TYPE XXXXXIII (P10)	81-129						81-129
IL13RA64	IL13RA64	IL-13 RECEPTOR, TYPE XXXXXIV (P10)	81-129						81-129
IL13RA65	IL13RA65	IL-13 RECEPTOR, TYPE XXXXXV (P10)	81-129						81-129
IL13RA66	IL13RA66	IL-13 RECEPTOR, TYPE XXXXXVI (P10)	81-129						81-129
IL13RA67	IL13RA67	IL-13 RECEPTOR, TYPE XXXXXVII (P10)	81-129						81-129
IL13RA68	IL13RA68	IL-13 RECEPTOR, TYPE XXXXXVIII (P10)	81-129						81-129
IL13RA69	IL13RA69	IL-13 RECEPTOR, TYPE XXXXXIX (P10)	81-129						81-129
IL13RA70	IL13RA70	IL-13 RECEPTOR, TYPE XXXXXX (P10)	81-129						81-129
IL13RA71	IL13RA71	IL-13 RECEPTOR, TYPE XXXXXI (P10)	81-129						81-129
IL13RA72	IL13RA72	IL-13 RECEPTOR, TYPE XXXXXII (P10)	81-129						81-129
IL13RA73	IL13RA73	IL-13 RECEPTOR, TYPE XXXXXIII (P10)	81-129						81-129
IL13RA74	IL13RA74	IL-13 RECEPTOR, TYPE XXXXXIV (P10)	81-129						81-129
IL13RA75	IL13RA75	IL-13 RECEPTOR, TYPE XXXXXV (P10)	81-129						81-129
IL13RA76	IL13RA76	IL-13 RECEPTOR, TYPE XXXXXVI (P10)	81-129						81-129
IL13RA77	IL13RA77	IL-13 RECEPTOR, TYPE XXXXXVII (P10)	81-129						81-129
IL13RA78	IL13RA78	IL-13 RECEPTOR, TYPE XXXXXVIII (P10)	81-129						81-129
IL13RA79	IL13RA79	IL-13 RECEPTOR, TYPE XXXXXIX (P10)	81-129						81-129
IL13RA80	IL13RA80	IL-13 RECEPTOR, TYPE XXXXXX (P10)	81-129						81-129
IL13RA81	IL13RA81	IL-13 RECEPTOR, TYPE XXXXXI (P10)	81-129						81-129
IL13RA82	IL13RA82	IL-13 RECEPTOR, TYPE XXXXXII (P10)	81-129						81-129
IL13RA83	IL13RA83	IL-13 RECEPTOR, TYPE XXXXXIII (P10)	81-129						81-129
IL13RA84	IL13RA84	IL-13 RECEPTOR, TYPE XXXXXIV (P10)	81-129						81-129
IL13RA85	IL13RA85	IL-13 RECEPTOR, TYPE XXXXXV (P10)	81-129						81-129
IL13RA86	IL13RA86	IL-13 RECEPTOR, TYPE XXXXXVI (P10)	81-129						81-129
IL13RA87	IL13RA87	IL-13 RECEPTOR, TYPE XXXXXVII (P10)	81-129						81-129
IL13RA88	IL13RA88	IL-13 RECEPTOR, TYPE XXXXXVIII (P10)	81-129						81-129
IL13RA89	IL13RA89	IL-13 RECEPTOR, TYPE XXXXXIX (P10)	81-129						81-129
IL13RA90	IL13RA90	IL-13 RECEPTOR, TYPE XXXXXX (P10)	81-129						81-129
IL13RA91	IL13RA91	IL-13 RECEPTOR, TYPE XXXXXI (P10)	81-129						81-129
IL13RA92	IL13RA92	IL-13 RECEPTOR, TYPE XXXXXII (P10)	81-129						81-129
IL13RA93	IL13RA93	IL-13 RECEPTOR, TYPE XXXXXIII (P10)	81-129						81-129
IL13RA94	IL13RA94	IL-13 RECEPTOR, TYPE XXXXXIV (P10)	81-129						81-129
IL13RA95	IL13RA95	IL-13 RECEPTOR, TYPE XXXXXV (P10)	81-129						81-129
IL13RA96	IL13RA96	IL-13 RECEPTOR, TYPE XXXXXVI (P10)	81-129						81-129
IL13RA97	IL13RA97	IL-13 RECEPTOR, TYPE XXXXXVII (P10)	81-129						81-129
IL13RA98	IL13RA98	IL-13 RECEPTOR, TYPE XXXXXVIII (P10)	81-129						81-129
IL13RA99	IL13RA99	IL-13 RECEPTOR, TYPE XXXXXIX (P10)	81-129						81-129
IL13RA100	IL13RA100	IL-13 RECEPTOR, TYPE XXXXXX (P10)	81-129						81-129
IL13RA101	IL13RA101	IL-13 RECEPTOR, TYPE XXXXXI (P10)	81-129						81-129
IL13RA102	IL13RA102	IL-13 RECEPTOR, TYPE XXXXXII (P10)	81-129						81-129
IL13RA103	IL13RA103	IL-13 RECEPTOR, TYPE XXXXXIII (P10)	81-129						81-129
IL13RA104	IL13RA104	IL-13 RECEPTOR, TYPE XXXXXIV (P10)	81-129						81-129
IL13RA105	IL13RA105	IL-13 RECEPTOR, TYPE XXXXXV (P10)	81-129						81-129
IL13RA106	IL13RA106	IL-13 RECEPTOR, TYPE XXXXXVI (P10)	81-129						81-129
IL13RA107	IL13RA107	IL-13 RECEPTOR, TYPE XXXXXVII (P10)	81-129						81-129
IL13RA108	IL13RA108	IL-13 RECEPTOR, TYPE XXXXXVIII (P10)	81-129						81-129
IL13RA109	IL13RA109	IL-13 RECEPTOR, TYPE XXXXXIX (P10)	81-129						81-129
IL13RA110	IL13RA110	IL-13 RECEPTOR, TYPE XXXXXX (P10)	81-129						81-129
IL13RA111	IL13RA111	IL-13 RECEPTOR, TYPE XXXXXI (P10)	81-129						81-129
IL13RA112	IL13RA112	IL-13 RECEPTOR, TYPE XXXXXII (P10)	81-129						81-129
IL13RA113	IL13RA113	IL-13 RECEPTOR, TYPE XXXXXIII (P10)	81-129						81-129
IL13RA114	IL13RA114	IL-13 RECEPTOR, TYPE XXXXXIV (P10)	81-129						81-129
IL13RA115	IL13RA115	IL-13 RECEPTOR, TYPE XXXXXV (P10)	81-129						81-129
IL13RA116	IL13RA116	IL-13 RECEPTOR, TYPE XXXXXVI (P10)	81-129						81-129
IL13RA117	IL13RA117	IL-13 RECEPTOR, TYPE XXXXXVII (P10)	81-129						81-129
IL13RA118	IL13RA118	IL-13 RECEPTOR, TYPE XXXXXVIII (P10)	81-129						81-129
IL13RA119	IL13RA119	IL-13 RECEPTOR, TYPE XXXXXIX (P10)	81-129						81-129
IL13RA120	IL13RA120	IL-13 RECEPTOR, TYPE XXXXXX (P10)	81-129						81-129
IL13RA121	IL13RA121	IL-13 RECEPTOR, TYPE XXXXXI (P10)	81-129						81-129
IL13RA122	IL13RA122	IL-13 RECEPTOR, TYPE XXXXXII (P10)	81-129						81-129
IL13RA123	IL13RA123	IL-13 RECEPTOR, TYPE XXXXXIII (P10)	81-129						81-129
IL13RA124	IL13RA124	IL-13 RECEPTOR, TYPE XXXXXIV (P10)	81-129						81-129
IL13RA125	IL13RA125	IL-13 RECEPTOR, TYPE XXXXXV (P10)	81-129						81-129
IL13RA126	IL13RA126	IL-13 RECEPTOR, TYPE XXXXXVI (P10)	81-129						81-129
IL13RA127	IL13RA127	IL-13 RECEPTOR, TYPE XXXXXVII (P10)	81-129						81-129
IL13RA128	IL13RA128	IL-13 RECEPTOR, TYPE XXXXXVIII (P10)	81-129						81-129
IL13RA129	IL13RA129	IL-13 RECEPTOR, TYPE XXXXXIX (P10)	81-129						81-129
IL13RA130	IL13RA130	IL-13 RECEPTOR, TYPE XXXXXX (P10)	81-129						81-129
IL13RA131	IL13RA131	IL-13 RECEPTOR, TYPE XXXXXI (P10)	81-129						81-129
IL13RA132	IL13RA132	IL-13 RECEPTOR, TYPE XXXXXII (P10)	81-129						81-129
IL13RA133	IL13RA133	IL-13 RECEPTOR, TYPE XXXXXIII (P10)	81-129						81-129
IL13RA134	IL13RA134	IL-13 RECEPTOR, TYPE XXXXXIV (P10)	81-129						81-129
IL13RA135	IL13RA135	IL-13 RECEPTOR, TYPE XXXXXV (P10)	81-129						81-129
IL13RA136	IL13RA136	IL-13 RECEPTOR, TYPE XXXXXVI (P10)	81-129						81-129
IL13RA137	IL13RA137	IL-13 RECEPTOR, TYPE XXXXXVII (P10)	81-129						81-129
IL13RA138	IL13RA138	IL-13 RECEPTOR, TYPE XXXXXVIII (P10)	81-129						

[illegible]

PROTEIN	1971-1974	1975-1978	1979-1982	1983-1986	1987-1990	1991-1994	1995-1998	1999-2002	2003-2006	2007-2010	2011-2014	2015-2018	2019-2022	2023-2026	2027-2030	2031-2034	2035-2038	2039-2042	2043-2046	2047-2050	2051-2054	2055-2058	2059-2062	2063-2066	2067-2070	2071-2074	2075-2078	2079-2082	2083-2086	2087-2090	2091-2094	2095-2098	2099-2102	2103-2106	2107-2110	2111-2114	2115-2118	2119-2122	2123-2126	2127-2130	2131-2134	2135-2138	2139-2142	2143-2146	2147-2150	2151-2154	2155-2158	2159-2162	2163-2166	2167-2170	2171-2174	2175-2178	2179-2182	2183-2186	2187-2190	2191-2194	2195-2198	2199-2202	2203-2206	2207-2210	2211-2214	2215-2218	2219-2222	2223-2226	2227-2230	2231-2234	2235-2238	2239-2242	2243-2246	2247-2250	2251-2254	2255-2258	2259-2262	2263-2266	2267-2270	2271-2274	2275-2278	2279-2282	2283-2286	2287-2290	2291-2294	2295-2298	2299-2302	2303-2306	2307-2310	2311-2314	2315-2318	2319-2322	2323-2326	2327-2330	2331-2334	2335-2338	2339-2342	2343-2346	2347-2350	2351-2354	2355-2358	2359-2362	2363-2366	2367-2370	2371-2374	2375-2378	2379-2382	2383-2386	2387-2390	2391-2394	2395-2398	2399-2402	2403-2406	2407-2410	2411-2414	2415-2418	2419-2422	2423-2426	2427-2430	2431-2434	2435-2438	2439-2442	2443-2446	2447-2450	2451-2454	2455-2458	2459-2462	2463-2466	2467-2470	2471-2474	2475-2478	2479-2482	2483-2486	2487-2490	2491-2494	2495-2498	2499-2502	2503-2506	2507-2510	2511-2514	2515-2518	2519-2522	2523-2526	2527-2530	2531-2534	2535-2538	2539-2542	2543-2546	2547-2550	2551-2554	2555-2558	2559-2562	2563-2566	2567-2570	2571-2574	2575-2578	2579-2582	2583-2586	2587-2590	2591-2594	2595-2598	2599-2602	2603-2606	2607-2610	2611-2614	2615-2618	2619-2622	2623-2626	2627-2630	2631-2634	2635-2638	2639-2642	2643-2646	2647-2650	2651-2654	2655-2658	2659-2662	2663-2666	2667-2670	2671-2674	2675-2678	2679-2682	2683-2686	2687-2690	2691-2694	2695-2698	2699-2702	2703-2706	2707-2710	2711-2714	2715-2718	2719-2722	2723-2726	2727-2730	2731-2734	2735-2738	2739-2742	2743-2746	2747-2750	2751-2754	2755-2758	2759-2762	2763-2766	2767-2770	2771-2774	2775-2778	2779-2782	2783-2786	2787-2790	2791-2794	2795-2798	2799-2802	2803-2806	2807-2810	2811-2814	2815-2818	2819-2822	2823-2826	2827-2830	2831-2834	2835-2838	2839-2842	2843-2846	2847-2850	2851-2854	2855-2858	2859-2862	2863-2866	2867-2870	2871-2874	2875-2878	2879-2882	2883-2886	2887-2890	2891-2894	2895-2898	2899-2902	2903-2906	2907-2910	2911-2914	2915-2918	2919-2922	2923-2926	2927-2930	2931-2934	2935-2938	2939-2942	2943-2946	2947-2950	2951-2954	2955-2958	2959-2962	2963-2966	2967-2970	2971-2974	2975-2978	2979-2982	2983-2986	2987-2990	2991-2994	2995-2998	2999-3002	3003-3006	3007-3010	3011-3014	3015-3018	3019-3022	3023-3026	3027-3030	3031-3034	3035-3038	3039-3042	3043-3046	3047-3050	3051-3054	3055-3058	3059-3062	3063-3066	3067-3070	3071-3074	3075-3078	3079-3082	3083-3086	3087-3090	3091-3094	3095-3098	3099-3102	3103-3106	3107-3110	3111-3114	3115-3118	3119-3122	3123-3126	3127-3130	3131-3134	3135-3138	3139-3142	3143-3146	3147-3150	3151-3154	3155-3158	3159-3162	3163-3166	3167-3170	3171-3174	3175-3178	3179-3182	3183-3186	3187-3190	3191-3194	3195-3198	3199-3202	3203-3206	3207-3210	3211-3214	3215-3218	3219-3222	3223-3226	3227-3230	3231-3234	3235-3238	3239-3242	3243-3246	3247-3250	3251-3254	3255-3258	3259-3262	3263-3266	3267-3270	3271-3274	3275-3278	3279-3282	3283-3286	3287-3290	3291-3294	3295-3298	3299-3302	3303-3306	3307-3310	3311-3314	3315-3318	3319-3322	3323-3326	3327-3330	3331-3334	3335-3338	3339-3342	3343-3346	3347-3350	3351-3354	3355-3358	3359-3362	3363-3366	3367-3370	3371-3374	3375-3378	3379-3382	3383-3386	3387-3390	3391-3394	3395-3398	3399-3402	3403-3406	3407-3410	3411-3414	3415-3418	3419-3422	3423-3426	3427-3430	3431-3434	3435-3438	3439-3442	3443-3446	3447-3450	3451-3454	3455-3458	3459-3462	3463-3466	3467-3470	3471-3474	3475-3478	3479-3482	3483-3486	3487-3490	3491-3494	3495-3498	3499-3502	3503-3506	3507-3510	3511-3514	3515-3518	3519-3522	3523-3526	3527-3530	3531-3534	3535-3538	3539-3542	3543-3546	3547-3550	3551-3554	3555-3558	3559-3562	3563-3566	3567-3570	3571-3574	3575-3578	3579-3582	3583-3586	3587-3590	3591-3594	3595-3598	3599-3602	3603-3606	3607-3610	3611-3614	3615-3618	3619-3622	3623-3626	3627-3630	3631-3634	3635-3638	3639-3642	3643-3646	3647-3650	3651-3654	3655-3658	3659-3662	3663-3666	3667-3670	3671-3674	3675-3678	3679-3682	3683-3686	3687-3690	3691-3694	3695-3698	3699-3702	3703-3706	3707-3710	3711-3714	3715-3718	3719-3722	3723-3726	3727-3730	3731-3734	3735-3738	3739-3742	3743-3746	3747-3750	3751-3754	3755-3758	3759-3762	3763-3766	3767-3770	3771-3774	3775-3778	3779-3782	3783-3786	3787-3790	3791-3794	3795-3798	3799-3802	3803-3806	3807-3810	3811-3814	3815-3818	3819-3822	3823-3826	3827-3830	3831-3834	3835-3838	3839-3842	3843-3846	3847-3850	3851-3854	3855-3858	3859-3862	3863-3866	3867-3870	3871-3874	3875-3878	3879-3882	3883-3886	3887-3890	3891-3894	3895-3898	3899-3902	3903-3906	3907-3910	3911-3914	3915-3918	3919-3922	3923-3926	3927-3930	3931-3934	3935-3938	3939-3942	3943-3946	3947-3950	3951-3954	3955-3958	3959-3962	3963-3966	3967-3970	3971-3974	3975-3978	3979-3982	3983-3986	3987-3990	3991-3994	3995-3998	3999-4002	4003-4006	4007-4010	4011-4014	4015-4018	4019-4022	4023-4026	4027-4030	4031-4034	4035-4038	4039-4042	4043-4046	4047-4050	4051-4054	4055-4058	4059-4062	4063-4066	4067-4070	4071-4074	4075-4078	4079-4082	4083-4086	4087-4090	4091-4094	4095-4098	4099-4102	4103-4106	4107-4110	4111-4114	4115-4118	4119-4122	4123-4126	4127-4130	4131-4134	4135-4138	4139-4142	4143-4146	4147-4150	4151-4154	4155-4158	4159-4162	4163-4166	4167-4170	4171-4174	4175-4178	4179-4182	4183-4186	4187-4190	4191-4194	4195-4198	4199-4202	4203-4206	4207-4210	4211-4214	4215-4218	4219-4222	4223-4226	4227-4230	4231-4234	4235-4238	4239-4242	4243-4246	4247-4250	4251-4254	4255-4258	4259-4262	4263-4266	4267-4270	4271-4274	4275-4278	4279-4282	4283-4286	4287-4290	4291-4294	4295-4298	4299-4302	4303-4306	4307-4310	4311-4314	4315-4318	4319-4322	4323-4326	4327-4330	4331-4334	4335-4338	4339-4342	4343-4346	4347-4350	4351-4354	4355-4358	4359-4362	4363-4366	4367-4370	4371-4374	4375-4378	4379-4382	4383-4386	4387-4390	4391-4394	4395-4398	4399-4402	4403-4406	4407-4410	4411-4414	4415-4418	4419-4422	4423-4426	4427-4430	4431-4434	4435-4438	4439-4442	4443-4446	4447-4450	4451-4454	4455-4458	4459-4462	4463-4466	4467-4470	4471-4474	4475-4478	4479-4482	4483-4486	4487-4490	4491-4494	4495-4498	4499-4502	4503-4506	4507-4510	4511-4514	4515-4518	4519-4522	4523-4526	4527-4530	4531-4534	4535-4538	4539-4542	4543-4546	4547-4550	4551-4554	4555-4558	4559-4562	4563-4566	4567-4570	4571-4574	4575-4578	4579-4582	4583-4586	4587-4590	4591-4594	4595-4598	4599-4602	4603-4606	4607-4610	4611-4614	4615-4618	4619-4622	4623-4626	4627-4630	4631-4634	4635-4638	4639-4642	4643-4646	4647-4650	4651-4654	4655-4658	4659-4662	4663-4666	4667-4670	4671-4674	4675-4678	4679-4682	4683-4686	4687-4690	4691-4694	4695-4698	4699-4702	4703-4706	4707-4710	4711-4714	4715-4718	4719-4722	4723-4726	4727-4730	4731-4734	4735-4738	4739-4742	4743-4746	4747-4750	4751-4754	4755-4758	4759-4762	4763-4766	4767-4770	4771-4774	4775-4778	4779-4782	4783-4786	4787-4790	4791-4794	4795-4798	4799-4802	4803-4806	4807-4810	4811-4814	4815-4818	4819-4822	4823-4826	4827-4830	4831-4834	4835-4838	4839-4842	4843-4846	4847-4850	4851-4854	4855-4858	4859-4862	4863-4866	4867-4870	4871-4874	4875-4878	4879-4882	4883-4886	4887-4890	4891-4894	4895-4898	4899-4902	4903-4906	4907-4910	4911-4914	4915-4918	4919-4922	4923-4926	4927-4930	4931-4934	4935-4938	4939-4942	4943-4946	4947-4950	4951-4954	4955-4958	4959-4962	4963-4966	4967-4970	4971-4974	4975-4978	4979-4982	4983-4986	4987-4990	4991-4994	4995-4998	4999-5002	5003-5006	5007-5010	5011-5014	5015-5018	5019-5022	5023-5026	5027-5030	5031-5034	5035-5038	5039-5042	5043-5046	5047-5050	5051-5054	5055-5058	5059-5062	5063-5066	5067-5070	5071-5074	5075-5078	5079-5082	5083-5086	5087-5090	5091-5094	5095-5098	5099-5102	5103-5106	5107-5110	5111-5114	5115-5118	5119-5122	5123-5126	5127-5130	5131-5134	5135-5138	5139-5142	5143-5146	5147-5150	5151-5154	5155-5158	5159-5162	5163-5166	5167-5170	5171-5174	5175-5178	5179-5182	5183-5186	5187-5190	5191-5194	5195-5198	5199-5202	5203-5206	5207-5210	5211-5214	5215-5218	5219-5222	5223-5226	5227-5230	5231-5234	5235-5238	5239-5242	5243-5246	5247-5250	5251-5254	5255-5258	5259-5262	5263-5266	5267-5270	5271-5274	5275-5278	5279-5282	5283-5286	5287-5290	5291-5294	5295-5298	5299-5302	5303-5306	5307-5310	5311-5314	5315-5318	5319-5322	5323-5326	5327-5330	5331-5334	5335-5338	5339-5342	5343-5346	5347-5350	5351-5354	5355-5358	5359-5362	5363-5366	5367-5370	5371-5374	5375-5378	5379-5382	5383-5386	5387-5390	5391-5394	5395-5398	5399-5402	5403-5406	5407-5410	5411-5414	5415-5418	5419-5422	5423-5426	5427-5430	5431-5434	5435-5438	5439-5442	5443-5446	5447-5450	5451-5454	5455-5458	5459-5462	5463-5466	5467-5470	5471-5474
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[illegible]

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PCGENE	19717566 Motif Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13
FILE NAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13
P100 HUMAN	60S RIBOSOMAL PROTEIN L3	142-192												
P101 HUMAN	60S RIBOSOMAL PROTEIN L3	18-163												
P102 HUMAN	60S RIBOSOMAL PROTEIN L3	18-163												
P103 HUMAN	57 KD RO PROTEIN (SODIUM SYNDROME TYPE A ANTIGEN (SS-A))	192-253												
P104 HUMAN	40 KD RO PROTEIN (SODIUM SYNDROME TYPE A ANTIGEN (SS-A))	192-253												
P105 HUMAN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C1 (HNRNP C1) AND HNRNP	16-43												
P106 HUMAN	HETEROGENEOUS RIBONUCLEOPROTEIN L (HNRNP L)	501-538												
P107 HUMAN	HETEROGENEOUS RIBONUCLEOPROTEIN U	630-637												
P108 HUMAN	DNA-DIRECTED RNA POLYMERASE II 175 KD POLYPEPTIDE	249-296	663-720	879-906	1114-1141	1171-1198								
P109 HUMAN	DNA-DIRECTED RNA POLYMERASE II 140 KD POLYPEPTIDE	636-667	1008-1015											
P110 HUMAN	DNA-DIRECTED RNA POLYMERASE II 133 KD POLYPEPTIDE	243-274												
P111 HUMAN	RETINOIC ACID RECEPTOR RXR-ALPHA	318-332												
P112 HUMAN	RETINOIC ACID RECEPTOR RXR-BETA ISOFORM 1	376-403												
P113 HUMAN	RETINOIC ACID RECEPTOR RXR-BETA ISOFORM 2	396-423												
P114 HUMAN	RETINOIC ACID RECEPTOR RXR-BETA ISOFORM 3	60-87												
P115 HUMAN	60S RIBOSOMAL PROTEIN S12	89-116												
P116 HUMAN	60S RIBOSOMAL PROTEIN S16	26-51												
P117 HUMAN	60S RIBOSOMAL PROTEIN S17A	14-41												
P118 HUMAN	60S RIBOSOMAL PROTEIN S17A	31-100												
P119 HUMAN	60S RIBOSOMAL PROTEIN S17B	116-161												
P120 HUMAN	60S RIBOSOMAL PROTEIN S8	121-150												
P121 HUMAN	60S RIBOSOMAL PROTEIN TCG1	11-47												
P122 HUMAN	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A (UI SNRNP A PROTEIN)	17-48												
P123 HUMAN	UI SMALL NUCLEAR RIBONUCLEOPROTEIN B	154-188	493-532	866-893	2790-2777	2820-2847	3104-3131	3129-3156	3012-3019	4021-4048				
P124 HUMAN	RYANODINE RECEPTOR, SKELETAL MUSCLE	12-34												
P125 HUMAN	5-100 PROTEIN, ALPHA CHAIN	14-36												
P126 HUMAN	5-100 PROTEIN, BETA CHAIN	31-38												
P127 HUMAN	5-100 PROTEIN	389-416												
P128 HUMAN	ADENOSYLMONOCYSTEINASE (EC 3.3.1.15) (ADENOSYL-L-HOMOCYSTEINE	209-236												
P129 HUMAN	DNA-BINDING PROTEIN SATB1	78-103												
P130 HUMAN	SQUAMOUS CELL CARCINOMA ANTIGEN (SCCA) (PROTEIN TA-A)	72-101												
P131 HUMAN	STEM CELL FACTOR PRECURSOR (SCF)	84-98												
P132 HUMAN	STEM CELL FACTOR PRECURSOR (SCF) (CONTAINS SEXUAL BASIC	176-226	288-239	314-368										
P133 HUMAN	STEM CELL FACTOR PRECURSOR (SCF) (CONTAINS SEXUAL BASIC	101-226	304-335	403-439	519-535									
P134 HUMAN	STEM CELL FACTOR PRECURSOR (SCF) (CONTAINS SEXUAL BASIC	38-45	134-181											
P135 HUMAN	SET PROTEIN	146-178												
P136 HUMAN	SECRETORY GRANIN I PRECURSOR (CHROMOGRANIN B)	290-317	314-361											
P137 HUMAN	SECRETORY GRANIN II PRECURSOR (CHROMOGRANIN C)	84-113	151-193	316-283										
P138 HUMAN	BONE SIALOPROTEIN II PRECURSOR (BSP II)	211-238	543-572											
P139 HUMAN	POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L	418-441												
P140 HUMAN	SKI-RELATED ONCOGENE SHON	193-220	570-621	651-712	1099-1126	1461-1502	1812-1909	1981-2022	2120-2154	2273-2350				
P141 HUMAN	SPECTRIN ALPHA CHAIN	2146-2171												
P142 HUMAN	SPECTRIN BETA CHAIN, ERYTHROCYTE	150-177	316-330	346-370	648-673	987-1021	1037-1093	1187-1224	1307-1374	1834-1861				
P143 HUMAN	SEPIA TENDIN REDUCTASE (EC 1.1.1.153) (SPR)	90-124												
P144 HUMAN	SERUM RESPONSE FACTOR (SRF)	76-110	480-507											
P145 HUMAN	SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT (SR-ALPHA)	289-316												
P146 HUMAN	SODIUM STATIN RECEPTOR TYPE 1	47-74												
P147 HUMAN	STATIN (PHOSPHOPROTEIN P19) (ONCOPROTEIN P19) (LEUKEMIA-ASSOCIATED	1748-1755												
P148 HUMAN	SUCRASE-ISOMALTAZE, INTESTINAL (EC 3.2.1.48) (EC 3.2.1.10)	31-47												
P149 HUMAN	SYNAPTOSOMAL PROTEIN 1	44-71												
P150 HUMAN	ASPARTYL-TRNA SYNTHETASE ALPHA-2 SUBUNIT (EC 6.1.1.13) (ASPARTATE-	170-201	240-271											
P151 HUMAN	MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE (CONTAINS GLUTAMYL-TRN	180-442	468-502											
P152 HUMAN	HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE-TRNA LIGASE)	140-167	250-277											
P153 HUMAN	SYNAPTOTAGMIN 1 (PS)	497-524	638-683											
P154 HUMAN	THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE-TRNA	230-257	413-440											
P155 HUMAN	VALYL-TRNA SYNTHETASE (EC 6.1.1.9) (VALINE-TRNA LIGASE) (VALRS)	91-137	186-233											
P156 HUMAN	TRYPTOPANYL-TRNA SYNTHETASE (EC 6.1.1.3) (TRYPTOPHAN-TRNA LIGASE)	14-48	241-272											
P157 HUMAN	TRANSCRIPTION INITIATION FACTOR IIE-BETA CHAIN (TFIIE-BETA)	169-196												
P158 HUMAN	TRANSCRIPTION FACTOR AP-2 (FRAGMENT)													

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PCGENE	1071754 Modl Search on All Human Protein Sequences	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
FILE NAME	PROTEIN	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9
P20C HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-B CELLS (XERODERMA PIGMENTOSUM)	264-291								
P20C HUMAN	DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM)	81-110	1047-1081							
P20C HUMAN	DNA-REPAIR PROTEIN XPC-H	27-57								
P20C HUMAN	DNA-REPAIR PROTEIN XPC-H	27-56								
P210 HUMAN	ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1) (FLAGMENT)	17-62	1071-1078		1407-1500	2013-2037	2146-2180			
P210 HUMAN	ZINC FINGER PROTEIN 40 (HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENTIANCE-R)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 41 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 42 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 43 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 44 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 45 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 46 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 47 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 48 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 49 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 50 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 51 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 52 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 53 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 54 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 55 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 56 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 57 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 58 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 59 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 60 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 61 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 62 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 63 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 64 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 65 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 66 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 67 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 68 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 69 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 70 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 71 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 72 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 73 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 74 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 75 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 76 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 77 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 78 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 79 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 80 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 81 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 82 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 83 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 84 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 85 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 86 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 87 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 88 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 89 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 90 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 91 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 92 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 93 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 94 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 95 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 96 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 97 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 98 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 99 (HRC1744) (FLAGMENT)	17-62								
P210 HUMAN	ZINC FINGER PROTEIN 100 (HRC1744) (FLAGMENT)	17-62								

TABLE X

**Search Results Summary for PCTLZIP,
P1CTLZIP, and P2CTLZIP Motifs**

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PVQL2 CVRFS	442-467		PHEMA IAME9	221-237	231-247		PHEMA IANTO	321-338
PVQL2 CVRPU	440-466	604-619	PHEMA IAMN	86-101			PHEMA IANUR	321-338
PVQL2 CVRPR	216-233		PHEMA IANT6	237-263			PHEMA IAJAP	317-334
PVQL2 CVRPM	218-233		PHEMA IAGU7	221-237			PHEMA IAMAA	316-336
PVQL2 IBV6	1066-1071		PHEMA IARUD	234-260			PHEMA IAMAB	324-341
PVQL2 IBV8	1066-1070		PHEMA IABE2	234-260			PHEMA IAMAO	322-339
PVQL2 IBVD2	1066-1071		PHEMA IASH2	234-260			PHEMA IAME1	322-339
PVQL2 IBVK	1066-1070		PHEMA IASTA	230-246			PHEMA IAME2	322-339
PVQL2 IBVM	1066-1070		PHEMA IATAI	235-261			PHEMA IAME6	306-323
PVQL8 HSBVA	701-716		PHEMA IATKM	234-260			PHEMA IAMON	316-333
PVQL8 PRVJP	203-216		PHEMA IATKO	233-246			PHEMA IANT6	322-339
PVQL8 HSBVC	476-490		PHEMA IATKR	230-246			PHEMA IAPIL	330-337
PVQLC HSBV4	444-469		PHEMA IATRW	220-246			PHEMA IAGU7	306-323
PVQLC HSBV8	437-442		PHEMA IAUO	237-263			PHEMA IARUD	320-337
PVQLC PRVIF	446-461		PHEMA IAU89	235-261			PHEMA IABE2	320-337
PVQLD HSBV11	76-84		PHEMA IAV17	238-264			PHEMA IABH2	321-338
PVQLD HSBV2	76-84		PHEMA IAXIA	235-261			PHEMA IABTA	316-332
PVQLF BRVVA	285-280		PHEMA IAZCO	237-263			PHEMA IATKM	320-337
PVQLF BRVVC	285-280		PHEMA IAZH2	221-237			PHEMA IAUO	322-339
PVQLF BRVVR	285-280		PHEMA IAZH3	221-237			PHEMA IAV17	322-340
PVQLF HRSV1	285-280		PHEMA IAZUK	237-263			PHEMA IAZCO	322-339
PVQLF HRSVA	285-280		PHEMA IZBAA	116-131	286-310		PHEMA IAZH2	306-323
PVQLF HRSVL	285-280		PHEMA IZB8E	123-139	303-316		PHEMA IAZH3	306-323
PVQLF HRSVR	285-280		PHEMA IZBBO	116-132	293-308		PHEMA IAZUK	322-339
PVQLF MUMPS	8-84		PHEMA IZBFI	123-139	301-316		PHEMA MUMPM	101-118
PVQLI VZVD	276-293		PHEMA IZBFI	108-124	286-301		PHEMA MUMPR	101-118
PVQLM HANTB	800-816		PHEMA IZBGL	116-138	286-311		PHEMA NDVA	93-110
PVQLM PTPV	743-768		PHEMA IZBHK	116-132	293-308		PHEMA NDVB	93-110
PVQLM SECUR	801-816		PHEMA IZBIB	108-124	286-303		PHEMA NDVD	93-110
PVQLM SECUR	800-816		PHEMA IZBID	120-136	286-314		PHEMA NDVH	93-110
PVQLY LABBQ	426-441		PHEMA IZBLE	123-139	302-317		PHEMA NDVI	93-110
PVQLY LABBJ	427-442		PHEMA IZBMO	113-129	282-307		PHEMA NDVM	93-110
PVQLY MOPEI	426-440		PHEMA IZBME	116-132	286-311		PHEMA NDVQ	93-110
PVMS3 REOVD	521-536		PHEMA IZBNA	108-124	288-303		PHEMA NDVTO	93-110
PVMS4 HPSB8	380-396		PHEMA IZBOR	123-139	301-316		PHEMA NDVU	93-110
PVMS4 HPSB8	187-202		PHEMA IZBBI	123-139	301-316		PHEMA PHODV	36-63
PVMS4 WHV1	376-393		PHEMA IZBSJ	116-136	286-313		PHEMA P11HW	466-603
PVMS4 WHV6	383-398		PHEMA IZBUS	116-132	284-309		PHEMA P13B	111-128
PVMS4 WHV7	383-398		PHEMA IZBYI	116-132	286-311		PHEMA P13H4	111-128
PVMS4 WHV8	383-398		PHEMA IZBVK	123-139	303-318		PHEMA P13HA	111-128
PVMS4 WHV8I	383-398		PHEMA IZBYB	108-124	286-301		PHEMA P13HT	111-128
PVMS4 WHVW6	234-248		PHEMA MUMPM	133-148			PHEMA P13HU	111-128
PVMT2 IANIN	26-40		PHEMA MUMPR	133-148			PHEMA P13HV	111-128
PVMT2 IABAN	26-40		PHEMA MUMPS	133-148			PHEMA P13HW	111-128
PVMT2 IAPOW	26-40		PHEMA P11HW	466-603			PHEMA P13HX	111-128
PVMT2 IAPPR	26-40		PHEMA P13H	95-81			PHEMA P13HA	86-67
PVMT2 IAPFW	26-40		PHEMA P13HT	86-81				

PVMT2 IALE1	26-40	PHEMA P13B	324-340				PHEMA 8V41	86-102	
PVMT2 IALE2	26-40	PHEMA P13H4	324-340				PHEMA 8V5	84-101	
PVMT2 IAHAN	26-40	PHEMA P13VA	324-340				PHEMA 8V6CM	84-101	
PVMT2 IAPUE	26-40	PHEMA P13HT	324-340				PHEMA 8V6CP	84-101	
PVMT2 IABIN	26-40	PHEMA P13HU	324-340				PHEMA 8V6LN	84-101	
PVMT2 IAUDD	26-40	PHEMA P13HV	324-340				PVFO5 VACCC	280-297	
PVMT2 IAWIL	26-40	PHEMA P13HW	324-340				PVFO5 VACCP	280-297	
PVMT8 MYXVL	226-241	PHEMA P13HX	324-340				PVFO5 VACCV	281-288	
		PHEMA RINDK	306-383				PVFO5 VACCC	176-193	
		PHEMA 8V8	7-84				PVFO5 VACCV	176-193	
		PHEMA 8V6CM	7-84				PVQ27 HBVA	206-226	
		PHEMA 8V6CP	7-84				PVQ28 HBVI	173-190	
		PHEMA 8V6LN	7-84				PVQ35 HBVI	646-668	
		PVENV DRVH	42-57				PVQ43 HBVI	108-128	621-638
		PVENV EAV	28-41				PVQ67 HBVI	171-188	
		PVFT2 FOPPV	88-104				PVQ72 HBVI	1252-1268	
		PVFT7 CAPVK	88-104				PVQF1 HBVB	3073-3080	
		PVR05 VACCS	72-87				PVQL3 HBVB	1084-1111	
		PVQ01 HBVB	188-184				PVQLB HBVE1	736-763	
		PVQ01 HBVEB	208-225				PVQLB HBVE4	676-682	
		PVQ08 HBVI	134-148			317-332	PVQLB HBVEA	736-783	
		PVQ10 HBVA	108-124				PVQLB HBVEB	736-783	
		PVQ11 HBVI	103-118				PVQLB HBVEL	736-783	
		PVQ12 HBVI	270-288				PVQLB ILTV8	697-814	
		PVQ1 8PV1R	76-92				PVQLB ILTV8	607-824	
		PVQ20 HBVI	20-35				PVQLB ILTVT	607-824	
		PVQ06 BPOX2	22-37				PVQLC PRVF	180-187	
		PVQ36 HBVA	108-123				PVQLE VZVD	489-488	
		PVQ37 HBVI	284-288				PVOLF 8V5	401-418	
		PVQ41 HBVI	244-260				PVQLH HCMVA	388-382	
		PVQ46 HBVI	1244-1260				PVQLH HCMVT	384-381	
		PVQ55 HBVI	22-37			143-158	PVQLH HBVI1	246-282	803-820
		PVQ56 HBVI	288-283				PVQLH HBVI1E	246-282	803-820
		PVQ58 HBVI	101-117				PVQLI HBVI1	43-80	
		PVQ59 HBVA	190-146			330-346	PVQLM BUNL7	61-88	
		PVQ65 HBVI	267-282				PVQLM BUNBH	81-88	
		PVQ68 HBVI	382-378			618-633	PVQLM PUTJNH	712-728	
		PVQ71 HBVA	88-105				PVQLM PUUMB	712-728	
		PVQ8 BPH2	234-240				PVQLM RVFV	344-361	
		PVQ8 BPFZA	234-240				PVQLM RVFVZ	344-361	
		PVQ8 8PV1R	67-72				PVQLY LA98Q	12-84	
		PVQF1 HBVB	2210-2228				PVQLY LA88J	12-84	
		PVQL2 CV8P	123-138			174-180	PVQLY LYCVA	12-84	
		PVQL2 CV8L6	123-138			174-180	PVQLY LYCVW	12-84	
		PVQL2 CV8LY	123-138			174-180	PVQLY MOPEI	12-84	
		PVQL2 CV8M	123-138			174-180	PVMT REOVD	280-287	
		PVQL2 CV8Q	31-47			123-138	PVMT REOVL	280-287	

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[illegible]

PVMT2 IAFPR	28-40
PVMT2 IAFPW	28-40
PVMT2 IALE1	28-40
PVMT2 IALE2	28-40
PVMT2 IAMAN	28-40
PVMT2 IAPUE	28-40
PVMT2 IASIN	28-40
PVMT2 IAUDO	28-40
PVMT2 IAWIL	28-40
PVMT6 MYXVL	27B-2A1

TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP,
P5CTLZIP, and P6CTLZIP Motifs

PVMO1 VACCV	183-101	128-144	PVQL3 CVM4	909-1018		PVENV THOOV	368-378		PHENA P12H	13-34	
PVM1 REOVD	227-246		PVQL2 CVM4	947-988		PVQ01 VACCV	288-318		PHENA P12H	13-34	
PVM1 REOVL	227-246		PVQL3 CVM4H	968-977		PVQ01 VACCV	237-267		PHENA SV8	7-28	378-400
PVMAT HREVA	44-62		PVQL2 CVF8	84-83	1030-1067	PVQ01 VARV	288-318		PHENA SV6CM	7-28	378-400
PVMAT NDVA	180-208		PVQL2 CVPU	84-83	1030-1066	PVQ06 VACCC	31-61		PHENA SV6CP	7-28	378-400
PVMAT NDVB	180-208		PVQL2 CVPR8	814-833		PVQ06 VARV	31-61		PHENA SV6LN	7-28	378-400
PVMP CAMVC	183-201		PVQL2 CVPRM	814-833		PVQ06 BPFF1	26-46		PVQ01 HSV8	188-180	
PVMP CAMVD	183-201		PVQL2 FIPV	1041-1080		PVQ12 HSVII	161-171		PVQ01 HSVII	188-180	
PVMP CAMVE	183-201		PVQL2 IBV8	688-807	771-780	PVQ22 HSVII	300-320		PVQ23 HSVII	314-336	
PVMP CAMVN	183-201		PVQL2 IBV8	688-807	770-780	PVQ38 HSVII	848-868		PVQ37 BPOX2	86-88	
PVMP CAMVS	183-201		PVQL2 IBVD2	688-807	771-780	PVQ51 HSVII	28-49		PVQ43 HSVII	167-178	
PVMP CAMVW	183-201		PVQL2 IBVK	687-808	770-780	PVQ63 HSVII	338-368		PVQ55 HSVII	288-309	
PVMP FHYD	180-188		PVQL2 IBVM	687-808	770-780	PVQ65 HSVII	117-137		PVQ56 HSVII	86-100	
			PVQL8 HCMVA	708-726		PVQ74 HSV5A	124-144		PVQ58 HSVII	1165-1178	
			PVQL8 HCMVT	707-728		PVQL2 IBV8	328-348		PVQ58 HSVII	206-287	
			PVQL8 HSV8U	117-138		PVQL2 IBV8	327-347		PVQ60 HSVII	30-61	
			PVQL8 ILTV8	268-276		PVQL2 IBVD2	328-348		PVQ63 HSVII	238-268	
			PVQL8 ILTVS	268-285		PVQL2 IBVD3	328-348		PVQ61 IBV8	1868-1877	
			PVQL8 ILTVT	268-286		PVQL2 IBVK	327-347		PVQ63 HCMVA	167-178	
			PVQLC HSV11	3-94	467-488	PVQL2 IBVM	327-347	378-388	PVQL2 CVBF	1288-1280	
			PVQLC HSV1K	3-94	467-488	PVQL2 IBVU2	310-330		PVQL2 CVBL8	1288-1280	
			PVQLC HSVBC	476-494		PVQL8 EBV	732-752		PVQL2 CVBLV	1288-1280	
			PVQLC CHAV	438-466		PVQLB HCMVA	750-770		PVQL2 CVBM	1288-1280	
			PVQL8 RABVH	372-391		PVQLB HCMVT	761-771		PVQL2 CVBQ	1288-1280	
			PVQL8 HSV8	44-83		PVQLB HSV23	78-88		PVQL2 CVBV	1288-1280	
			PVQL1 VZVD	278-287		PVQLB HSV23	78-88		PVQL2 CVM4	1317-1338	
			PVQLM BUNGE	117-138		PVQLB HSV28	85-85		PVQL3 CVM4S	1288-1288	
			PVQLM PHV	152-171		PVQLB HSV8U	72-82		PVQL2 CVMJH	1178-1197	
			PVQLM PTPV	897-1019		PVQLB HSV82	278-288		PVQL8 HSV11	83-104	
			PVQLM PUUMH	166-174		PVQLB MCMV8	738-768		PVQL8 HSV1F	82-103	
			PVQLM PUUMS	166-174		PVQLF P13H4	283-303		PVQL8 HSV1K	83-103	
			PVQLM RVFV	830-848		PVQLG RABVE	454-474		PVQL8 HSV1P	83-104	
			PVQLM RVFV2	830-848		PVQLG RABVH	454-474		PVQL8 MCMV3	136-160	
			PVQLM UUK	855-874		PVQLG RABVP	454-474		PVQLC PRVF	448-487	
			PVQLY LYCVW	88-108		PVQLG RABVP	454-474		PVQLF CDVO	338-367	
			PVQNB CMV	1166-1104		PVQLG RABV	454-474		PVQLF MEAB1	224-246	
			PVM3 REOVD	521-640		PVQLG RABVT	454-474		PVQLF MEABY	227-248	
			PVME1 CVBM	171-180		PVQLH MCMV8	870-880		PVQLF MEABY	227-246	
			PVME1 CVH22	136-166		PVQLM BUNL7	1328-1348		PVQLF MUMPM	448-487	
			PVME1 CUPF8	174-183		PVQLM BUNH	1328-1348		PVQLF MUMPM	448-487	
			PVME1 CUPPU	174-183		PVQLM BUNYH	898-1018		PVQLF MUMPM	448-487	
			PVME1 CVPRM	174-183		PVQLM HANTH	898-1018		PVQLF PHOOV	308-328	
			PVME1 CVTKE	171-180		PVQLM HANTH	1000-1020		PVQLF P11HC	468-471	
						PVQLM HANTL	1001-1021		PVQLF P12H	468-471	
						PVQLM HANTV	1001-1021		PVQLF P12H	468-471	
						PVQLM RVFVZ	1168-1178		PVQLF P12H	468-471	
						PVQLM SEOUR	1000-1020		PVQLF P138	468-474	

	PVGLM 8C0US	809-1018	PVGLF PLH4	463-474
	PVGLM UKK	826-845	PVGLF RINDX	220-261
	PVGLY LYCA	12-32	PVGLF RINDL	220-241
	PVGLY LYCVW	12-32	PVOLF BENDG	460-481
	PVGLY PIARV	12-32	PVOLF BENDE	460-481
	PVGNB CMNV	141-161	PVOLF BENDH	460-481
	PVMAT MUMPS	310-330	PVOLF BENDJ	460-481
	PVMAT NDVA	308-329	PVOLF BENDZ	460-481
	PVMAT NDVB	308-329	PVOLF BV41	463-474
	PVMAT PIZHT	308-328	PVOLF SV8	446-467
	PVMAT PI4HA	312-332	PVGLH HCMVA	681-712
	PVMAT PI4HB	312-332	PVGLH HCMVT	680-711
	PVMAT SV41	308-328	PVGLH HVE4	304-326
	PVMAT SV6	308-328	PVGLH HVEB	287-318
	PVME1 IBV6	74-84	PVGLH HBVA	668-678
	PVME1 IBVB	74-84	PVGLI HBV2	2-23
	PVME1 IBVB2	74-84	PVGLI HSV23	2-23
	PVME1 IBVK	74-84	PVGLM BUNGE	187-218
	PVMSA HPBD8	201-221	PVGLM BUNL7	180-211
	PVMSA HPB08	208-228	PVGLM BUNSH	180-211
	PVMSA HPBHE	283-313	PVGLM SUNYW	183-214
	PVMSA WHV1	207-227	PVGLY LAB8Q	237-258
	PVMSA WHV69	212-232	PVGLY LAB8J	238-269
	PVMSA WHV7	212-232	PVQP8 EBV	87-88
	PVMSA WHV8	212-232	PVM01 VAGCC	281-302
	PVMSA WHV81	212-232	PVM01 VACCV	230-251
	PVMSA WHVW6	63-83	PVMAT HR8VA	189-190
			PVMAT RINDX	200-221
			PVMAT TRTV	123-143
			PVME1 CYNOC	64-85
			PVMSA HPBDB	201-222
			PVMSA HPBV0	70-91
			PVMSA HPBV2	244-266
			PVMSA HPBV4	244-265
			PVMSA HPBV6	244-268
			PVMSA HPBV8	233-284
			PVMSA HPBV0	70-91
			PVMSA HPBV1	233-264
			PVMSA HPBVJ	233-284
			PVMSA HPBVL	233-284
			PVMSA HPBVN	70-91
			PVMSA HPBV0	233-264
			PVMSA HPBVU	244-266
			PVMSA HPBVR	244-285
			PVMSA HPBV8	70-91"
			PVMSA HPBVW	233-254
			PVMSA HPBVY	233-254

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TABLE XII

Search Results Summary for P7CTLZIP,
P8CTLZIP, and P9CTLZIP Motifs

PCT/ZIP	LIBRARY FILE	PCT/ZIP	LIBRARY FILE	PCT/ZIP	LIBRARY FILE	PCT/ZIP	LIBRARY FILE
PENV BAEVA	303-224	PENV FR3FV	380-403	PENV BLVAF	303-327		
PENV HV1B1	488-620	PENV2 FR3FV	380-403	PENV BLVAU	303-327		
PENV HV1B6	483-616	PENV BIV06	178-201	PENV BLVAV	303-327		
PENV HV1B8	484-616	PENV BIV27	202-230	PENV BLVB2	303-327		
PENV HV1B9	603-626	PENV FOAMV	864-887	PENV BLVB8	303-327		
PENV HV1EL	485-617	PENV HV123	176-188	PENV BLVJ	303-327		
PENV HV1H2	488-620	PENV HV28E	3-28	PENV FIVPE	781-805		
PENV HV1H3	488-620	PENV HV2CA	760-773	PENV FIVSD	778-803		
PENV HV1J3	610-632	PENV HV2D1	3-28	PENV FIVT2	780-804		
PENV HV1JR	480-612	PENV HV2G1	772-785	PHEMA CVBLY	381-415		
PENV HV1K8	604-626	PENV HV2NZ	777-800	PHEMA CVBM	381-416		
PENV HV1MA	600-622	PENV JSRV	641-664	PHEMA CVBQ	381-416		
PENV HV1MF	486-616	PENV 8FV1	884-887	PHEMA CVHOC	381-416		
PENV HV1ND	488-610	PENV 8FV3L	861-904	PHEMA INCCA	442-486		
PENV HV1PV	488-620	PENV 8IVM1	603-626	PHEMA INCEN	430-484		
PENV HV1R1	488-611	PENV 8IVM2	602-625	PHEMA INCOL	430-484		
PENV HV1Z2	123-146	PENV 8IVM4	601-624	PHEMA INCY	428-483		
PENV HV1Z6	487-616	PENV 8IVB4	606-629	PHEMA INCJH	443-487		
PENV HV1Z8	606-627	PENV 8IVSP	610-633	PHEMA INCKY	428-483		
PENV HV1ZH	488-620	PHEMA COVO	200-223	PHEMA INCM1	428-483		
PENV JSRV	376-388	PHEMA P12H	66-88	PHEMA INCM2	428-483		
PENV MPBV	213-235	PHEMA P12HT	66-88	PHEMA INCP1	430-484		
PENV SRV1	213-235	PVF11 VACCC	181-184	PHEMA INCP2	430-484		
PHEMA IADIC	37-68	PVF16 VACCC	26-48	PHEMA INCP3	430-484		
PHEMA IADAN	21-43	PVF18 VACCP	3-28	PHEMA INCTA	430-484		
PHEMA IAD3	37-68	PVG11 AMEPV	313-338	PHEMA INCTA	430-484		
PHEMA IADH2	21-43	PVG28 H8V11	481-614	PHEMA MUMPM	101-126		
PHEMA IADH3	21-43	PVG43 H8V11	322-346	PHEMA MUMPR	101-126		
PHEMA IADH4	21-43	PVG52 H8V11	228-262	PHEMA MUMPS	101-126		
PHEMA IADH8	21-43	PVG87 H8V11	722-746	PHEMA PIHNV	28-63		
PHEMA IADH7	21-43	PVG12 CVBF	10-33	PENV BEV	82-98		
PHEMA IADH2	37-68	PVG13 CVBL9	681-674	PVF05 VACCC	280-304		
PHEMA IADMA	28-60	PVG13 CVBL1	10-33	PVF08 VACCP	280-304		
PHEMA IADU3	37-68	PVG13 CYMA4	1287-1280	PVF08 VACCV	281-306		
PHEMA IADN6	37-68	PVG13 CYMA6	1216-1238	PVF09 VACCC	176-200		
PHEMA IADN7	37-68	PVG13 CYMAH	1126-1148	PVF09 VACCV	176-200		
PHEMA IADN8	37-68	PVG13 CVPF8	1274-1287	PVG01 VZVD	68-82		
PHEMA IADN9	37-68	PVG13 CVPPU	1222-1285	PVG10 H8V8A	365-378		
PHEMA IADN10	37-68	PVG13 CVPR8	1060-1073	PVG12 H8V8A	68-82		
PHEMA IADN11	37-68	PVG13 CVPRM	1060-1073	PVG18 H8V11	88-112		
PHEMA IADN12	37-68	PVG13 CVPRM	1277-1300	PVG28 H8V11	172-187		
PHEMA IADN13	37-68	PVG13 F8V	188-218	PVG43 H8V11	108-133		
PHEMA IADN14	37-68	PVG13 H8V8	188-218	PVG87 H8V11	108-132		
PHEMA IADN15	37-68	PVG13 H8V8	188-218	PVG72 H8V11	720-744		
PHEMA IADN16	37-68	PVG13 H8V2	188-218	PVG51 H8V8	3801-3828		
PHEMA IADN17	37-68	PVG13 H8V3	188-218				
PHEMA IADN18	37-68	PVG13 H8V4	188-218				
PHEMA IADN19	37-68	PVG13 H8V5	188-218				
PHEMA IADN20	37-68	PVG13 H8V6	188-218				
PHEMA IADN21	37-68	PVG13 H8V7	188-218				
PHEMA IADN22	37-68	PVG13 H8V8	188-218				
PHEMA IADN23	37-68	PVG13 H8V9	188-218				
PHEMA IADN24	37-68	PVG13 H8V10	188-218				
PHEMA IADN25	37-68	PVG13 H8V11	188-218				
PHEMA IADN26	37-68	PVG13 H8V12	188-218				
PHEMA IADN27	37-68	PVG13 H8V13	188-218				
PHEMA IADN28	37-68	PVG13 H8V14	188-218				
PHEMA IADN29	37-68	PVG13 H8V15	188-218				
PHEMA IADN30	37-68	PVG13 H8V16	188-218				
PHEMA IADN31	37-68	PVG13 H8V17	188-218				
PHEMA IADN32	37-68	PVG13 H8V18	188-218				
PHEMA IADN33	37-68	PVG13 H8V19	188-218				
PHEMA IADN34	37-68	PVG13 H8V20	188-218				
PHEMA IADN35	37-68	PVG13 H8V21	188-218				
PHEMA IADN36	37-68	PVG13 H8V22	188-218				
PHEMA IADN37	37-68	PVG13 H8V23	188-218				
PHEMA IADN38	37-68	PVG13 H8V24	188-218				
PHEMA IADN39	37-68	PVG13 H8V25	188-218				
PHEMA IADN40	37-68	PVG13 H8V26	188-218				
PHEMA IADN41	37-68	PVG13 H8V27	188-218				
PHEMA IADN42	37-68	PVG13 H8V28	188-218				
PHEMA IADN43	37-68	PVG13 H8V29	188-218				
PHEMA IADN44	37-68	PVG13 H8V30	188-218				
PHEMA IADN45	37-68	PVG13 H8V31	188-218				
PHEMA IADN46	37-68	PVG13 H8V32	188-218				
PHEMA IADN47	37-68	PVG13 H8V33	188-218				
PHEMA IADN48	37-68	PVG13 H8V34	188-218				
PHEMA IADN49	37-68	PVG13 H8V35	188-218				
PHEMA IADN50	37-68	PVG13 H8V36	188-218				
PHEMA IADN51	37-68	PVG13 H8V37	188-218				
PHEMA IADN52	37-68	PVG13 H8V38	188-218				
PHEMA IADN53	37-68	PVG13 H8V39	188-218				
PHEMA IADN54	37-68	PVG13 H8V40	188-218				
PHEMA IADN55	37-68	PVG13 H8V41	188-218				
PHEMA IADN56	37-68	PVG13 H8V42	188-218				
PHEMA IADN57	37-68	PVG13 H8V43	188-218				
PHEMA IADN58	37-68	PVG13 H8V44	188-218				
PHEMA IADN59	37-68	PVG13 H8V45	188-218				
PHEMA IADN60	37-68	PVG13 H8V46	188-218				
PHEMA IADN61	37-68	PVG13 H8V47	188-218				
PHEMA IADN62	37-68	PVG13 H8V48	188-218				
PHEMA IADN63	37-68	PVG13 H8V49	188-218				
PHEMA IADN64	37-68	PVG13 H8V50	188-218				
PHEMA IADN65	37-68	PVG13 H8V51	188-218				
PHEMA IADN66	37-68	PVG13 H8V52	188-218				
PHEMA IADN67	37-68	PVG13 H8V53	188-218				
PHEMA IADN68	37-68	PVG13 H8V54	188-218				
PHEMA IADN69	37-68	PVG13 H8V55	188-218				
PHEMA IADN70	37-68	PVG13 H8V56	188-218				
PHEMA IADN71	37-68	PVG13 H8V57	188-218				
PHEMA IADN72	37-68	PVG13 H8V58	188-218				
PHEMA IADN73	37-68	PVG13 H8V59	188-218				
PHEMA IADN74	37-68	PVG13 H8V60	188-218				
PHEMA IADN75	37-68	PVG13 H8V61	188-218				
PHEMA IADN76	37-68	PVG13 H8V62	188-218				
PHEMA IADN77	37-68	PVG13 H8V63	188-218				
PHEMA IADN78	37-68	PVG13 H8V64	188-218				
PHEMA IADN79	37-68	PVG13 H8V65	188-218				
PHEMA IADN80	37-68	PVG13 H8V66	188-218				
PHEMA IADN81	37-68	PVG13 H8V67	188-218				
PHEMA IADN82	37-68	PVG13 H8V68	188-218				
PHEMA IADN83	37-68	PVG13 H8V69	188-218				
PHEMA IADN84	37-68	PVG13 H8V70	188-218				
PHEMA IADN85	37-68	PVG13 H8V71	188-218				
PHEMA IADN86	37-68	PVG13 H8V72	188-218				
PHEMA IADN87	37-68	PVG13 H8V73	188-218				
PHEMA IADN88	37-68	PVG13 H8V74	188-218				
PHEMA IADN89	37-68	PVG13 H8V75	188-218				
PHEMA IADN90	37-68	PVG13 H8V76	188-218				
PHEMA IADN91	37-68	PVG13 H8V77	188-218				
PHEMA IADN92	37-68	PVG13 H8V78	188-218				
PHEMA IADN93	37-68	PVG13 H8V79	188-218				
PHEMA IADN94	37-68	PVG13 H8V80	188-218				
PHEMA IADN95	37-68	PVG13 H8V81	188-218				
PHEMA IADN96	37-68	PVG13 H8V82	188-218				
PHEMA IADN97	37-68	PVG13 H8V83	188-218				
PHEMA IADN98	37-68	PVG13 H8V84	188-218				
PHEMA IADN99	37-68	PVG13 H8V85	188-218				
PHEMA IADN100	37-68	PVG13 H8V86	188-218				
PHEMA IADN101	37-68	PVG13 H8V87	188-218				
PHEMA IADN102	37-68	PVG13 H8V88	188-218				
PHEMA IADN103	37-68	PVG13 H8V89	188-218				
PHEMA IADN104	37-68	PVG13 H8V90	188-218				
PHEMA IADN105	37-68	PVG13 H8V91	188-218				
PHEMA IADN106	37-68	PVG13 H8V92	188-218				
PHEMA IADN107	37-68	PVG13 H8V93	188-218				
PHEMA IADN108	37-68	PVG13 H8V94	188-218				
PHEMA IADN109	37-68	PVG13 H8V95	188-218				
PHEMA IADN110	37-68	PVG13 H8V96	188-218				
PHEMA IADN111	37-68	PVG13 H8V97	188-218				
PHEMA IADN112	37-68	PVG13 H8V98	188-218				
PHEMA IADN113	37-68	PVG13 H8V99	188-218				
PHEMA IADN114	37-68	PVG13 H8V100	188-218				
PHEMA IADN115	37-68	PVG13 H8V101	188-218				
PHEMA IADN116	37-68	PVG13 H8V102	188-218				
PHEMA IADN117	37-68	PVG13 H8V103	188-218				
PHEMA IADN118	37-68	PVG13 H8V104	188-218				
PHEMA IADN119	37-68	PVG13 H8V105	188-218				
PHEMA IADN120	37-68	PVG13 H8V106	188-218				
PHEMA IADN121	37-68	PVG13 H8V107	188-218				
PHEMA IADN122	37-68	PVG13 H8V108	188-218				
PHEMA IADN123	37-68	PVG13 H8V109	188-218				
PHEMA IADN124	37-68	PVG13 H8V110	188-218				
PHEMA IADN125	37-68	PVG13 H8V111	188-218				
PHEMA IADN126	37-68	PVG13 H8V112	188-218				
PHEMA IADN127	37-68	PVG13 H8V113	188-218				
PHEMA IADN128	37-68	PVG13 H8V114	188-218				
PHEMA IADN129	37-68	PVG13 H8V115	188-218				
PHEMA IADN130	37-68	PVG13 H8V116	188-218				
PHEMA IADN131	37-68	PVG13 H8V117	188-218				
PHEMA IADN132	37-68	PVG13 H8V118	188-218				
PHEMA IADN133	37-68	PVG13 H8V119	188-218				
PHEMA IADN134	37-68	PVG13 H8V120	188-218				
PHEMA IADN135	37-68	PVG13 H8V121	188-218				
PHEMA IADN136	37-68	PVG13 H8V122	188-218				
PHEMA IADN137	37-68	PVG13 H8V123	188-218				
PHEMA IADN138	37-68	PVG13 H8V124	188-218				
PHEMA IADN139	37-68	PVG13 H8V125	188-218				
PHEMA IADN140	37-68	PVG13 H8V126	188-218				
PHEMA IADN141	37-68	PVG13 H8V127	188-218				
PHEMA IADN142	37-68	PVG13 H8V128	188-218				
PHEMA							

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TABLE XIII

SEARCH RESULTS SUMMARY FOR P12LZIPC MOTIF

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GENE		PROTEIN	AB Virus (No. Bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 453	AREA 454	AREA 455	AREA 456	AREA 457	AREA 458	AREA 459	AREA 460	AREA 461	AREA 462	AREA 463	AREA 464	AREA 465	AREA 466	AREA 467	AREA 468	AREA 469	AREA 470	AREA 471	AREA 472	AREA 473	AREA 474	AREA 475	AREA 476	AREA 477	AREA 478	AREA 479	AREA 480	AREA 481	AREA 482	AREA 483	AREA 484	AREA 485	AREA 486	AREA 487	AREA 488	AREA 489	AREA 490	AREA 491	AREA 492	AREA 493	AREA 494	AREA 495	AREA 496	AREA 497	AREA 498	AREA 499	AREA 500
PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31	PUL31																																																																																					

[illegible]

FCUNE	FUNCTION	AB VIEWS (No. Bacteriophages)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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	PROTEIN	GENE	P1CTD2IP	AB Virus (No Bacteriophage)	AREA1	AREA2	AREA3	AREA4	AREA5	AREA6	AREA7	AREA8	AREA9	AREA10	AREA11	AREA12	AREA13	AREA14	AREA15	AREA16	AREA17	AREA18	AREA19	AREA20	AREA21	AREA22	AREA23	AREA24	AREA25	AREA26	AREA27	AREA28	AREA29	AREA30	AREA31	AREA32	AREA33	AREA34	AREA35	AREA36	AREA37	AREA38	AREA39	AREA40	AREA41	AREA42	AREA43	AREA44	AREA45	AREA46	AREA47	AREA48	AREA49	AREA50	AREA51	AREA52	AREA53	AREA54	AREA55	AREA56	AREA57	AREA58	AREA59	AREA60	AREA61	AREA62	AREA63	AREA64	AREA65	AREA66	AREA67	AREA68	AREA69	AREA70	AREA71	AREA72	AREA73	AREA74	AREA75	AREA76	AREA77	AREA78	AREA79	AREA80	AREA81	AREA82	AREA83	AREA84	AREA85	AREA86	AREA87	AREA88	AREA89	AREA90	AREA91	AREA92	AREA93	AREA94	AREA95	AREA96	AREA97	AREA98	AREA99	AREA100	AREA101	AREA102	AREA103	AREA104	AREA105	AREA106	AREA107	AREA108	AREA109	AREA110	AREA111	AREA112	AREA113	AREA114	AREA115	AREA116	AREA117	AREA118	AREA119	AREA120	AREA121	AREA122	AREA123	AREA124	AREA125	AREA126	AREA127	AREA128	AREA129	AREA130	AREA131	AREA132	AREA133	AREA134	AREA135	AREA136	AREA137	AREA138	AREA139	AREA140	AREA141	AREA142	AREA143	AREA144	AREA145	AREA146	AREA147	AREA148	AREA149	AREA150	AREA151	AREA152	AREA153	AREA154	AREA155	AREA156	AREA157	AREA158	AREA159	AREA160	AREA161	AREA162	AREA163	AREA164	AREA165	AREA166	AREA167	AREA168	AREA169	AREA170	AREA171	AREA172	AREA173	AREA174	AREA175	AREA176	AREA177	AREA178	AREA179	AREA180	AREA181	AREA182	AREA183	AREA184	AREA185	AREA186	AREA187	AREA188	AREA189	AREA190	AREA191	AREA192	AREA193	AREA194	AREA195	AREA196	AREA197	AREA198	AREA199	AREA200	AREA201	AREA202	AREA203	AREA204	AREA205	AREA206	AREA207	AREA208	AREA209	AREA210	AREA211	AREA212	AREA213	AREA214	AREA215	AREA216	AREA217	AREA218	AREA219	AREA220	AREA221	AREA222	AREA223	AREA224	AREA225	AREA226	AREA227	AREA228	AREA229	AREA230	AREA231	AREA232	AREA233	AREA234	AREA235	AREA236	AREA237	AREA238	AREA239	AREA240	AREA241	AREA242	AREA243	AREA244	AREA245	AREA246	AREA247	AREA248	AREA249	AREA250	AREA251	AREA252	AREA253	AREA254	AREA255	AREA256	AREA257	AREA258	AREA259	AREA260	AREA261	AREA262	AREA263	AREA264	AREA265	AREA266	AREA267	AREA268	AREA269	AREA270	AREA271	AREA272	AREA273	AREA274	AREA275	AREA276	AREA277	AREA278	AREA279	AREA280	AREA281	AREA282	AREA283	AREA284	AREA285	AREA286	AREA287	AREA288	AREA289	AREA290	AREA291	AREA292	AREA293	AREA294	AREA295	AREA296	AREA297	AREA298	AREA299	AREA300	AREA301	AREA302	AREA303	AREA304	AREA305	AREA306	AREA307	AREA308	AREA309	AREA310	AREA311	AREA312	AREA313	AREA314	AREA315	AREA316	AREA317	AREA318	AREA319	AREA320	AREA321	AREA322	AREA323	AREA324	AREA325	AREA326	AREA327	AREA328	AREA329	AREA330	AREA331	AREA332	AREA333	AREA334	AREA335	AREA336	AREA337	AREA338	AREA339	AREA340	AREA341	AREA342	AREA343	AREA344	AREA345	AREA346	AREA347	AREA348	AREA349	AREA350	AREA351	AREA352	AREA353	AREA354	AREA355	AREA356	AREA357	AREA358	AREA359	AREA360	AREA361	AREA362	AREA363	AREA364	AREA365	AREA366	AREA367	AREA368	AREA369	AREA370	AREA371	AREA372	AREA373	AREA374	AREA375	AREA376	AREA377	AREA378	AREA379	AREA380	AREA381	AREA382	AREA383	AREA384	AREA385	AREA386	AREA387	AREA388	AREA389	AREA390	AREA391	AREA392	AREA393	AREA394	AREA395	AREA396	AREA397	AREA398	AREA399	AREA400	AREA401	AREA402	AREA403	AREA404	AREA405	AREA406	AREA407	AREA408	AREA409	AREA410	AREA411	AREA412	AREA413	AREA414	AREA415	AREA416	AREA417	AREA418	AREA419	AREA420	AREA421	AREA422	AREA423	AREA424	AREA425	AREA426	AREA427	AREA428	AREA429	AREA430	AREA431	AREA432	AREA433	AREA434	AREA435	AREA436	AREA437	AREA438	AREA439	AREA440	AREA441	AREA442	AREA443	AREA444	AREA445	AREA446	AREA447	AREA448	AREA449	AREA450	AREA451	AREA452	AREA453	AREA454	AREA455	AREA456	AREA457	AREA458	AREA459	AREA460	AREA461	AREA462	AREA463	AREA464	AREA465	AREA466	AREA467	AREA468	AREA469	AREA470	AREA471	AREA472	AREA473	AREA474	AREA475	AREA476	AREA477	AREA478	AREA479	AREA480	AREA481	AREA482	AREA483	AREA484	AREA485	AREA486	AREA487	AREA488	AREA489	AREA490	AREA491	AREA492	AREA493	AREA494	AREA495	AREA496	AREA497	AREA498	AREA499	AREA500	AREA501	AREA502	AREA503	AREA504	AREA505	AREA506	AREA507	AREA508	AREA509	AREA510	AREA511	AREA512	AREA513	AREA514	AREA515	AREA516	AREA517	AREA518	AREA519	AREA520	AREA521	AREA522	AREA523	AREA524	AREA525	AREA526	AREA527	AREA528	AREA529	AREA530	AREA531	AREA532	AREA533	AREA534	AREA535	AREA536	AREA537	AREA538	AREA539	AREA540	AREA541	AREA542	AREA543	AREA544	AREA545	AREA546	AREA547	AREA548	AREA549	AREA550	AREA551	AREA552	AREA553	AREA554	AREA555	AREA556	AREA557	AREA558	AREA559	AREA560	AREA561	AREA562	AREA563	AREA564	AREA565	AREA566	AREA567	AREA568	AREA569	AREA570	AREA571	AREA572	AREA573	AREA574	AREA575	AREA576	AREA577	AREA578	AREA579	AREA580	AREA581	AREA582	AREA583	AREA584	AREA585	AREA586	AREA587	AREA588	AREA589	AREA590	AREA591	AREA592	AREA593	AREA594	AREA595	AREA596	AREA597	AREA598	AREA599	AREA600	AREA601	AREA602	AREA603	AREA604	AREA605	AREA606	AREA607	AREA608	AREA609	AREA610	AREA611	AREA612	AREA613	AREA614	AREA615	AREA616	AREA617	AREA618	AREA619	AREA620	AREA621	AREA622	AREA623	AREA624	AREA625	AREA626	AREA627	AREA628	AREA629	AREA630	AREA631	AREA632	AREA633	AREA634	AREA635	AREA636	AREA637	AREA638	AREA639	AREA640	AREA641	AREA642	AREA643	AREA644	AREA645	AREA646	AREA647	AREA648	AREA649	AREA650	AREA651	AREA652	AREA653	AREA654	AREA655	AREA656	AREA657	AREA658	AREA659	AREA660	AREA661	AREA662	AREA663	AREA664	AREA665	AREA666	AREA667	AREA668	AREA669	AREA670	AREA671	AREA672	AREA673	AREA674	AREA675	AREA676	AREA677	AREA678	AREA679	AREA680	AREA681	AREA682	AREA683	AREA684	AREA685	AREA686	AREA687	AREA688	AREA689	AREA690	AREA691	AREA692	AREA693	AREA694	AREA695	AREA696	AREA697	AREA698	AREA699	AREA700	AREA701	AREA702	AREA703	AREA704	AREA705	AREA706	AREA707	AREA708	AREA709	AREA710	AREA711	AREA712	AREA713	AREA714	AREA715	AREA716	AREA717	AREA718	AREA719	AREA720	AREA721	AREA722	AREA723	AREA724	AREA725	AREA726	AREA727	AREA728	AREA729	AREA730	AREA731	AREA732	AREA733	AREA734	AREA735	AREA736	AREA737	AREA738	AREA739	AREA740	AREA741	AREA742	AREA743	AREA744	AREA745	AREA746	AREA747	AREA748	AREA749	AREA750	AREA751	AREA752	AREA753	AREA754	AREA755	AREA756	AREA757	AREA758	AREA759	AREA760	AREA761	AREA762	AREA763	AREA764	AREA765	AREA766	AREA767	AREA768	AREA769	AREA770	AREA771	AREA772	AREA773	AREA774	AREA775	AREA776	AREA777	AREA778	AREA779	AREA780	AREA781	AREA782	AREA783	AREA784	AREA785	AREA786	AREA787	AREA788	AREA789	AREA790	AREA791	AREA792	AREA793	AREA794	AREA795	AREA796	AREA797	AREA798	AREA799	AREA800	AREA801	AREA802	AREA803	AREA804	AREA805	AREA806	AREA807	AREA808	AREA809	AREA810	AREA811	AREA812	AREA813	AREA814	AREA815	AREA816	AREA817	AREA818	AREA819	AREA820	AREA821	AREA822	AREA823	AREA824	AREA825	AREA826	AREA827	AREA828	AREA829	AREA830	AREA831	AREA832	AREA833	AREA834	AREA835	AREA836	AREA837	AREA838	AREA839	AREA840	AREA841	AREA842	AREA843	AREA844	AREA845	AREA846	AREA847	AREA848	AREA849	AREA850	AREA851	AREA852	AREA853	AREA854	AREA855	AREA856	AREA857	AREA858	AREA859	AREA860	AREA861	AREA862	AREA863	AREA864	AREA865	AREA866	AREA867	AREA868	AREA869	AREA870	AREA871	AREA872	AREA873	AREA874	AREA875	AREA876	AREA877	AREA878	AREA879	AREA880	AREA881	AREA882	AREA883	AREA884	AREA885	AREA886	AREA887	AREA888	AREA889	AREA890	AREA891	AREA892	AREA893	AREA894	AREA895	AREA896	AREA897	AREA898	AREA899	AREA900	AREA901	AREA902	AREA903	AREA904	AREA905	AREA906	AREA907	AREA908	AREA909	AREA910	AREA911	AREA912	AREA913	AREA914	AREA915	AREA916	AREA917	AREA918	AREA919	AREA920	AREA921	AREA922	AREA923	AREA924	AREA925	AREA926	AREA927	AREA928	AREA929	AREA930	AREA931	AREA932	AREA933	AREA934	AREA935	AREA936	AREA937	AREA938	AREA939	AREA940	AREA941	AREA942	AREA943	AREA944	AREA945	AREA946	AREA947	AREA948	AREA949	AREA950	AREA951	AREA952	AREA953	AREA954	AREA955	AREA956	AREA957	AREA958	AREA959	AREA960	AREA961	AREA962	AREA963	AREA964	AREA965	AREA966	AREA967	AREA968	AREA969	AREA970	AREA971	AREA972	AREA973	AREA974	AREA975	AREA976	AREA977	AREA978	AREA979	AREA980	AREA981	AREA982	AREA983	AREA984	AREA985	AREA986	AREA987	AREA988	AREA989	AREA990	AREA991	AREA992	AREA993	AREA994	AREA995	AREA996	AREA997	AREA998	AREA999	AREA1000
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380

[illegible]

382

POSSIBLE	FUNCTION	ADJ. Virus (No Bacteriophage)	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5	AREA 6	AREA 7	AREA 8	AREA 9	AREA 10	AREA 11	AREA 12	AREA 13	AREA 14	AREA 15	AREA 16	AREA 17	AREA 18	AREA 19	AREA 20	AREA 21	AREA 22	AREA 23	AREA 24	AREA 25	AREA 26	AREA 27	AREA 28	AREA 29	AREA 30	AREA 31	AREA 32	AREA 33	AREA 34	AREA 35	AREA 36	AREA 37	AREA 38	AREA 39	AREA 40	AREA 41	AREA 42	AREA 43	AREA 44	AREA 45	AREA 46	AREA 47	AREA 48	AREA 49	AREA 50	AREA 51	AREA 52	AREA 53	AREA 54	AREA 55	AREA 56	AREA 57	AREA 58	AREA 59	AREA 60	AREA 61	AREA 62	AREA 63	AREA 64	AREA 65	AREA 66	AREA 67	AREA 68	AREA 69	AREA 70	AREA 71	AREA 72	AREA 73	AREA 74	AREA 75	AREA 76	AREA 77	AREA 78	AREA 79	AREA 80	AREA 81	AREA 82	AREA 83	AREA 84	AREA 85	AREA 86	AREA 87	AREA 88	AREA 89	AREA 90	AREA 91	AREA 92	AREA 93	AREA 94	AREA 95	AREA 96	AREA 97	AREA 98	AREA 99	AREA 100	AREA 101	AREA 102	AREA 103	AREA 104	AREA 105	AREA 106	AREA 107	AREA 108	AREA 109	AREA 110	AREA 111	AREA 112	AREA 113	AREA 114	AREA 115	AREA 116	AREA 117	AREA 118	AREA 119	AREA 120	AREA 121	AREA 122	AREA 123	AREA 124	AREA 125	AREA 126	AREA 127	AREA 128	AREA 129	AREA 130	AREA 131	AREA 132	AREA 133	AREA 134	AREA 135	AREA 136	AREA 137	AREA 138	AREA 139	AREA 140	AREA 141	AREA 142	AREA 143	AREA 144	AREA 145	AREA 146	AREA 147	AREA 148	AREA 149	AREA 150	AREA 151	AREA 152	AREA 153	AREA 154	AREA 155	AREA 156	AREA 157	AREA 158	AREA 159	AREA 160	AREA 161	AREA 162	AREA 163	AREA 164	AREA 165	AREA 166	AREA 167	AREA 168	AREA 169	AREA 170	AREA 171	AREA 172	AREA 173	AREA 174	AREA 175	AREA 176	AREA 177	AREA 178	AREA 179	AREA 180	AREA 181	AREA 182	AREA 183	AREA 184	AREA 185	AREA 186	AREA 187	AREA 188	AREA 189	AREA 190	AREA 191	AREA 192	AREA 193	AREA 194	AREA 195	AREA 196	AREA 197	AREA 198	AREA 199	AREA 200	AREA 201	AREA 202	AREA 203	AREA 204	AREA 205	AREA 206	AREA 207	AREA 208	AREA 209	AREA 210	AREA 211	AREA 212	AREA 213	AREA 214	AREA 215	AREA 216	AREA 217	AREA 218	AREA 219	AREA 220	AREA 221	AREA 222	AREA 223	AREA 224	AREA 225	AREA 226	AREA 227	AREA 228	AREA 229	AREA 230	AREA 231	AREA 232	AREA 233	AREA 234	AREA 235	AREA 236	AREA 237	AREA 238	AREA 239	AREA 240	AREA 241	AREA 242	AREA 243	AREA 244	AREA 245	AREA 246	AREA 247	AREA 248	AREA 249	AREA 250	AREA 251	AREA 252	AREA 253	AREA 254	AREA 255	AREA 256	AREA 257	AREA 258	AREA 259	AREA 260	AREA 261	AREA 262	AREA 263	AREA 264	AREA 265	AREA 266	AREA 267	AREA 268	AREA 269	AREA 270	AREA 271	AREA 272	AREA 273	AREA 274	AREA 275	AREA 276	AREA 277	AREA 278	AREA 279	AREA 280	AREA 281	AREA 282	AREA 283	AREA 284	AREA 285	AREA 286	AREA 287	AREA 288	AREA 289	AREA 290	AREA 291	AREA 292	AREA 293	AREA 294	AREA 295	AREA 296	AREA 297	AREA 298	AREA 299	AREA 300	AREA 301	AREA 302	AREA 303	AREA 304	AREA 305	AREA 306	AREA 307	AREA 308	AREA 309	AREA 310	AREA 311	AREA 312	AREA 313	AREA 314	AREA 315	AREA 316	AREA 317	AREA 318	AREA 319	AREA 320	AREA 321	AREA 322	AREA 323	AREA 324	AREA 325	AREA 326	AREA 327	AREA 328	AREA 329	AREA 330	AREA 331	AREA 332	AREA 333	AREA 334	AREA 335	AREA 336	AREA 337	AREA 338	AREA 339	AREA 340	AREA 341	AREA 342	AREA 343	AREA 344	AREA 345	AREA 346	AREA 347	AREA 348	AREA 349	AREA 350	AREA 351	AREA 352	AREA 353	AREA 354	AREA 355	AREA 356	AREA 357	AREA 358	AREA 359	AREA 360	AREA 361	AREA 362	AREA 363	AREA 364	AREA 365	AREA 366	AREA 367	AREA 368	AREA 369	AREA 370	AREA 371	AREA 372	AREA 373	AREA 374	AREA 375	AREA 376	AREA 377	AREA 378	AREA 379	AREA 380	AREA 381	AREA 382	AREA 383	AREA 384	AREA 385	AREA 386	AREA 387	AREA 388	AREA 389	AREA 390	AREA 391	AREA 392	AREA 393	AREA 394	AREA 395	AREA 396	AREA 397	AREA 398	AREA 399	AREA 400	AREA 401	AREA 402	AREA 403	AREA 404	AREA 405	AREA 406	AREA 407	AREA 408	AREA 409	AREA 410	AREA 411	AREA 412	AREA 413	AREA 414	AREA 415	AREA 416	AREA 417	AREA 418	AREA 419	AREA 420	AREA 421	AREA 422	AREA 423	AREA 424	AREA 425	AREA 426	AREA 427	AREA 428	AREA 429	AREA 430	AREA 431	AREA 432	AREA 433	AREA 434	AREA 435	AREA 436	AREA 437	AREA 438	AREA 439	AREA 440	AREA 441	AREA 442	AREA 443	AREA 444	AREA 445	AREA 446	AREA 447	AREA 448	AREA 449	AREA 450	AREA 451	AREA 452	AREA 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TABLE XIV

SEARCH RESULTS SUMMARY

FOR P23TLZIPC MOTIF

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	FUNCTION	PROTEIN	VIRUS	AREA1 38-59	AREA2 60-71	AREA3 72-83	AREA4 84-95	AREA5 96-107	AREA6 108-119	AREA7 120-131	AREA8 132-143	AREA9 144-155	AREA10 156-167	AREA11 168-179	AREA12 180-191	AREA13 192-203	AREA14 204-215	AREA15 216-227	AREA16 228-239	AREA17 240-251	AREA18 252-263	AREA19 264-275	AREA20 276-287	AREA21 288-299	AREA22 300-311	AREA23 312-323	AREA24 324-335	AREA25 336-347	AREA26 348-359	AREA27 360-371	AREA28 372-383	AREA29 384-395	AREA30 396-407	AREA31 408-419	AREA32 420-431	AREA33 432-443	AREA34 444-455	AREA35 456-467	AREA36 468-479	AREA37 480-491	AREA38 492-503	AREA39 504-515	AREA40 516-527	AREA41 528-539	AREA42 540-551	AREA43 552-563	AREA44 564-575	AREA45 576-587	AREA46 588-599	AREA47 600-611	AREA48 612-623	AREA49 624-635	AREA50 636-647	AREA51 648-659	AREA52 660-671	AREA53 672-683	AREA54 684-695	AREA55 696-707	AREA56 708-719	AREA57 720-731	AREA58 732-743	AREA59 744-755	AREA60 756-767	AREA61 768-779	AREA62 780-791	AREA63 792-803	AREA64 804-815	AREA65 816-827	AREA66 828-839	AREA67 840-851	AREA68 852-863	AREA69 864-875	AREA70 876-887	AREA71 888-899	AREA72 900-911	AREA73 912-923	AREA74 924-935	AREA75 936-947	AREA76 948-959	AREA77 960-971	AREA78 972-983	AREA79 984-995	AREA80 996-1007	AREA81 1008-1019	AREA82 1020-1031	AREA83 1032-1043	AREA84 1044-1055	AREA85 1056-1067	AREA86 1068-1079	AREA87 1080-1091	AREA88 1092-1103	AREA89 1104-1115	AREA90 1116-1127	AREA91 1128-1139	AREA92 1140-1151	AREA93 1152-1163	AREA94 1164-1175	AREA95 1176-1187	AREA96 1188-1199	AREA97 1200-1211	AREA98 1212-1223	AREA99 1224-1235	AREA100 1236-1247	AREA101 1248-1259	AREA102 1260-1271	AREA103 1272-1283	AREA104 1284-1295	AREA105 1296-1307	AREA106 1308-1319	AREA107 1320-1331	AREA108 1332-1343	AREA109 1344-1355	AREA110 1356-1367	AREA111 1368-1379	AREA112 1380-1391	AREA113 1392-1403	AREA114 1404-1415	AREA115 1416-1427	AREA116 1428-1439	AREA117 1440-1451	AREA118 1452-1463	AREA119 1464-1475	AREA120 1476-1487	AREA121 1488-1499	AREA122 1500-1511	AREA123 1512-1523	AREA124 1524-1535	AREA125 1536-1547	AREA126 1548-1559	AREA127 1560-1571	AREA128 1572-1583	AREA129 1584-1595	AREA130 1596-1607	AREA131 1608-1619	AREA132 1620-1631	AREA133 1632-1643	AREA134 1644-1655	AREA135 1656-1667	AREA136 1668-1679	AREA137 1680-1691	AREA138 1692-1703	AREA139 1704-1715	AREA140 1716-1727	AREA141 1728-1739	AREA142 1740-1751	AREA143 1752-1763	AREA144 1764-1775	AREA145 1776-1787	AREA146 1788-1799	AREA147 1800-1811	AREA148 1812-1823	AREA149 1824-1835	AREA150 1836-1847	AREA151 1848-1859	AREA152 1860-1871	AREA153 1872-1883	AREA154 1884-1895	AREA155 1896-1907	AREA156 1908-1919	AREA157 1920-1931	AREA158 1932-1943	AREA159 1944-1955	AREA160 1956-1967	AREA161 1968-1979	AREA162 1980-1991	AREA163 1992-2003	AREA164 2004-2015	AREA165 2016-2027	AREA166 2028-2039	AREA167 2040-2051	AREA168 2052-2063	AREA169 2064-2075	AREA170 2076-2087	AREA171 2088-2099	AREA172 2100-2111	AREA173 2112-2123	AREA174 2124-2135	AREA175 2136-2147	AREA176 2148-2159	AREA177 2160-2171	AREA178 2172-2183	AREA179 2184-2195	AREA180 2196-2207	AREA181 2208-2219	AREA182 2220-2231	AREA183 2232-2243	AREA184 2244-2255	AREA185 2256-2267	AREA186 2268-2279	AREA187 2280-2291	AREA188 2292-2303	AREA189 2304-2315	AREA190 2316-2327	AREA191 2328-2339	AREA192 2340-2351	AREA193 2352-2363	AREA194 2364-2375	AREA195 2376-2387	AREA196 2388-2399	AREA197 2400-2411	AREA198 2412-2423	AREA199 2424-2435	AREA200 2436-2447	AREA201 2448-2459	AREA202 2460-2471	AREA203 2472-2483	AREA204 2484-2495	AREA205 2496-2507	AREA206 2508-2519	AREA207 2520-2531	AREA208 2532-2543	AREA209 2544-2555	AREA210 2556-2567	AREA211 2568-2579	AREA212 2580-2591	AREA213 2592-2603	AREA214 2604-2615	AREA215 2616-2627	AREA216 2628-2639	AREA217 2640-26
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GENE	FUNCTION	AREA 1	AREA 2	AREA 3	AREA 4	AREA 5
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TABLE XV
RESPIRATORY SYNCYTIAL VIRUS DP107 F2 REGION ANALOG
CARBOXY TRUNCATIONS

	X-YTS-Z
	X-YTSV-Z
5	X-YTSVI-Z
	X-YTSVIT-Z
	X-YTSVITI-Z
	X-YTSVITIE-Z
	X-YTSVITIEL-Z
	X-YTSVITIELS-Z
	X-YTSVITIELSN-Z
10	X-YTSVITIELSNI-Z
	X-YTSVITIELSNIK-Z
	X-YTSVITIELSNIKE-Z
	X-YTSVITIELSNIKEN-Z
	X-YTSVITIELSNIKENK-Z
	X-YTSVITIELSNIKENKC-Z
	X-YTSVITIELSNIKENKCN-Z
	X-YTSVITIELSNIKENKCNG-Z
15	X-YTSVITIELSNIKENKCNGT-Z
	X-YTSVITIELSNIKENKCNGTD-Z
	X-YTSVITIELSNIKENKCNGTDA-Z
	X-YTSVITIELSNIKENKCNGTDAK-Z
	X-YTSVITIELSNIKENKCNGTDAKV-Z
	X-YTSVITIELSNIKENKCNGTDAKVK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKL-Z
20	X-YTSVITIELSNIKENKCNGTDAKVKLI-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQE-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQEL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELD-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKY-Z
25	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYK-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNA-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAV-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTE-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTEL-Z
30	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLL-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLM-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQ-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQS-Z
	X-YTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQST-Z

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The ne lett r amin acid code is used.

Additi nally,

"x" may r present an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxycarbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"z" may represent a carboxyl group; an amide group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVI
RESPIRATORY SYNCYTIAL VIRUS F2 DP178/DP107 REGION ANALOG
AMINO TRUNCATIONS

	X-QST-Z
	X-MQST-Z
5	X-LMQST-Z
	X-LLMQST-Z
	X-QLLMQST-Z
	X-LQLLMQST-Z
	X-ELQLLMQST-Z
	X-TELQLLMQST-Z
	X-VTELQLLMQST-Z
	X-AVTELQLLMQST-Z
10	X-NAVTELQLLMQST-Z
	X-KNAVTELQLLMQST-Z
	X-YKNAVTELQLLMQST-Z
	X-KYKNAVTELQLLMQST-Z
	X-DKYKNAVTELQLLMQST-Z
	X-LDKYKNAVTELQLLMQST-Z
	X-ELDKYKNAVTELQLLMQST-Z
15	X-QELDKYKNAVTELQLLMQST-Z
	X-KQELDKYKNAVTELQLLMQST-Z
	X-IKQELDKYKNAVTELQLLMQST-Z
	X-LIKQELDKYKNAVTELQLLMQST-Z
	X-KLIKQELDKYKNAVTELQLLMQST-Z
	X-VKLIKQELDKYKNAVTELQLLMQST-Z
	X-KVKLIKQELDKYKNAVTELQLLMQST-Z
20	X-AKVLIKQELDKYKNAVTELQLLMQST-Z
	X-DAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-GTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-CNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-KCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
25	X-KENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-NIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-LSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-IELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
30	X-TIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-ITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-VITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-SVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z
	X-TSVITIELSNIKENKCNGTDAKVLIKQELDKYKNAVTELQLLMQST-Z

The one letter amino acid code is used.

35 Additionally,

"x" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or t-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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"z" may represent a carboxyl group; an amido group; a t-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVII
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG
CARBOXY TRUNCATIONS

	X-FYD-Z
	X-FYDP-Z
	X-FYDPL-Z
5	X-FYDPLV-Z
	X-FYDPLVF-Z
	X-FYDPLVFP-Z
	X-FYDPLVFPS-Z
	X-FYDPLVFPSD-Z
	X-FYDPLVFPSDE-Z
	X-FYDPLVFPSDEF-Z
10	X-FYDPLVFPSDEFD-Z
	X-FYDPLVFPSDEFDA-Z
	X-FYDPLVFPSDEFDAS-Z
	X-FYDPLVFPSDEFDASI-Z
	X-FYDPLVFPSDEFDASIS-Z
	X-FYDPLVFPSDEFDASISQ-Z
	X-FYDPLVFPSDEFDASISQV-Z
	X-FYDPLVFPSDEFDASISQVN-Z
15	X-FYDPLVFPSDEFDASISQVNE-Z
	X-FYDPLVFPSDEFDASISQVNEK-Z
	X-FYDPLVFPSDEFDASISQVNEKI-Z
	X-FYDPLVFPSDEFDASISQVNEKIN-Z
	X-FYDPLVFPSDEFDASISQVNEKINQ-Z
	X-FYDPLVFPSDEFDASISQVNEKINQS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSL-Z
20	X-FYDPLVFPSDEFDASISQVNEKINQSLA-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAF-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFI-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIR-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRK-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKS-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSD-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDE-Z
25	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDEL-Z
	X-FYDPLVFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,

- 30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

- 35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier

group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XVIII
RESPIRATORY SYNCYTIAL VIRUS F1 DP178 REGION ANALOG
AMINO TRUNCATIONS

	X-DELL-Z
	X-SDELL-Z
5	X-KSDELL-Z
	X-RKSDELL-Z
	X-IRKSDELL-Z
	X-FIRKSDELL-Z
	X-AFIRKSDELL-Z
	X-LAFIRKSDELL-Z
	X-SLAFIRKSDELL-Z
10	X-QSLAFIRKSDELL-Z
	X-NQSLAFIRKSDELL-Z
	X-INQSLAFIRKSDELL-Z
	X-KINQSLAFIRKSDELL-Z
	X-EKINQSLAFIRKSDELL-Z
	X-NEKINQSLAFIRKSDELL-Z
	X-VNEKINQSLAFIRKSDELL-Z
	X-QVNEKINQSLAFIRKSDELL-Z
15	X-SQVNEKINQSLAFIRKSDELL-Z
	X-ISQVNEKINQSLAFIRKSDELL-Z
	X-SISQVNEKINQSLAFIRKSDELL-Z
	X-ASISQVNEKINQSLAFIRKSDELL-Z
	X-DASISQVNEKINQSLAFIRKSDELL-Z
	X-FDASISQVNEKINQSLAFIRKSDELL-Z
	X-EFDASISQVNEKINQSLAFIRKSDELL-Z
20	X-DEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-SDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-FPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-VFPSDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-LVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-PLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
	X-DPLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z
25	X-YDPLVFPDEFDASISQVNEKINQSLAFIRKSDELL-Z

The one letter amino acid code is used.

Additionally,

30 "X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxy, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

35 "Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XIX
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG
CARBOXY TRUNCATIONS

X-ITL-Z
 X-ITLN-Z
 X-ITLNN-Z
 5 X-ITLNN-S-Z
 X-ITLNN-SV-Z
 X-ITLNN-SVA-Z
 X-ITLNN-SVAL-Z
 X-ITLNN-SVALD-Z
 X-ITLNN-SVALDP-Z
 X-ITLNN-SVALDPI-Z
 10 X-ITLNN-SVALDPID-Z
 X-ITLNN-SVALDPIDI-Z
 X-ITLNN-SVALDPIDIS-Z
 X-ITLNN-SVALDPIDISI-Z
 X-ITLNN-SVALDPIDISIE-Z
 X-ITLNN-SVALDPIDISIEL-Z
 X-ITLNN-SVALDPIDISIELN-Z
 X-ITLNN-SVALDPIDISIELNK-Z
 15 X-ITLNN-SVALDPIDISIELNKA-Z
 X-ITLNN-SVALDPIDISIELNKAK-Z
 X-ITLNN-SVALDPIDISIELNKAKS-Z
 X-ITLNN-SVALDPIDISIELNKAKSD-Z
 X-ITLNN-SVALDPIDISIELNKAKSDL-Z
 X-ITLNN-SVALDPIDISIELNKAKSDLE-Z
 X-ITLNN-SVALDPIDISIELNKAKSDLEE-Z
 X-ITLNN-SVALDPIDISIELNKAKSDLEES-Z
 20 X-ITLNN-SVALDPIDISIELNKAKSDLEESK-Z
 X-ITLNN-SVALDPIDISIELNKAKSDLEESKE-Z
 X-ITLNN-SVALDPIDISIELNKAKSDLEESKEW-Z
 X-ITLNN-SVALDPIDISIELNKAKSDLEESKEWI-Z
 X-ITLNN-SVALDPIDISIELNKAKSDLEESKEWIR-Z
 X-ITLNN-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z

25 The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group,
 including but not limited to carbobenzoxyl, dansyl, or
 T-butyloxycarbonyl; an acetyl group; a 9-
 30 fluorenylmethoxy-carbonyl (Fmoc) group; a
 macromolecular carrier group including but not limited
 to lipid-fatty acid conjugates, polyethylene glycol,
 or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a
 T-butyloxycarbonyl group; a macromolecular carrier
 group including but not limited to lipid-fatty acid
 35 conjugates, polyethylene glycol, or carbohydrates.

TABLE XX
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP178 ANALOG
AMINO TRUNCATIONS

	X-RRS-Z
	X-IRRS-Z
5	X-WIRRS-Z
	X-EWIRRS-Z
	X-KEWIRRS-Z
	X-SKEWIRRS-Z
	X-ESKEWIRRS-Z
	X-EESKEWIRRS-Z
	X-LEESKEWIRRS-Z
10	X-DLEESKEWIRRS-Z
	X-SDLEESKEWIRRS-Z
	X-KSDLEESKEWIRRS-Z
	X-AKSDLEESKEWIRRS-Z
	X-KAKSDLEESKEWIRRS-Z
	X-NKAKSDLEESKEWIRRS-Z
	X-LNKAKSDLEESKEWIRRS-Z
	X-ELNKAKSDLEESKEWIRRS-Z
15	X-IELNKAKSDLEESKEWIRRS-Z
	X-SIELNKAKSDLEESKEWIRRS-Z
	X-ISIELNKAKSDLEESKEWIRRS-Z
	X-DISIELNKAKSDLEESKEWIRRS-Z
	X-IDISIELNKAKSDLEESKEWIRRS-Z
	X-PIDISIELNKAKSDLEESKEWIRRS-Z
	X-DPIDISIELNKAKSDLEESKEWIRRS-Z
20	X-LDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-ALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-VALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-SVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-NNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
	X-LNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z
25	X-TLNNSVALDPIDISIELNKAKSDLEESKEWIRRS-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a
 30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid
 35 conjugates, polyethylene glycol, or carbohydrates.

TABLE XXI
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG
CARBOXY TRUNCATIONS

X-ALG-Z
 X-ALGV-Z
 X-ALGVA-Z
 5 X-ALGVAT-Z
 X-ALGVATS-Z
 X-ALGVATSA-Z
 X-ALGVATSAQ-Z
 X-ALGVATSAQI-Z
 X-ALGVATSAQIT-Z
 X-ALGVATSAQITA-Z
 10 X-ALGVATSAQITAA-Z
 X-ALGVATSAQITA-AV-Z
 X-ALGVATSAQITA-AVA-Z
 X-ALGVATSAQITA-AVAL-Z
 X-ALGVATSAQITA-AVALV-Z
 X-ALGVATSAQITA-AVALVE-Z
 X-ALGVATSAQITA-AVALVEA-Z
 X-ALGVATSAQITA-AVALVEAK-Z
 15 X-ALGVATSAQITA-AVALVEAKQ-Z
 X-ALGVATSAQITA-AVALVEAKQA-Z
 X-ALGVATSAQITA-AVALVEAKQAR-Z
 X-ALGVATSAQITA-AVALVEAKQARS-Z
 X-ALGVATSAQITA-AVALVEAKQARSD-Z
 X-ALGVATSAQITA-AVALVEAKQARSDI-Z
 X-ALGVATSAQITA-AVALVEAKQARSDIE-Z
 20 X-ALGVATSAQITA-AVALVEAKQARSDIEK-Z
 X-ALGVATSAQITA-AVALVEAKQARSDIEKL-Z
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLK-Z
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKE-Z
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKEA-Z
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKEAI-Z
 X-ALGVATSAQITA-AVALVEAKQARSDIEKLKEAIR-Z

25 The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a
 30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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TABLE XXII
HUMAN PARAINFLUENZA VIRUS 3 F1 REGION DP107 ANALOG
AMINO TRUNCATIONS

	X-IRD-Z
	X-AIRD-Z
5	X-EAIRD-Z
	X-KEAIRD-Z
	X-LKEAIRD-Z
	X-KLKEAIRD-Z
	X-EKLKEAIRD-Z
	X-IEKLKEAIRD-Z
	X-DIEKLKEAIRD-Z
10	X-SDIEKLKEAIRD-Z
	X-RSDIEKLKEAIRD-Z
	X-ARSDIEKLKEAIRD-Z
	X-QARSDIEKLKEAIRD-Z
	X-KQARSDIEKLKEAIRD-Z
	X-AKQARSDIEKLKEAIRD-Z
	X-EAKQARSDIEKLKEAIRD-Z
	X-VEAKQARSDIEKLKEAIRD-Z
15	X-LVEAKQARSDIEKLKEAIRD-Z
	X-ALVEAKQARSDIEKLKEAIRD-Z
	X-VALVEAKQARSDIEKLKEAIRD-Z
	X-AVALVEAKQARSDIEKLKEAIRD-Z
	X-AAVALVEAKQARSDIEKLKEAIRD-Z
	X-TAAVALVEAKQARSDIEKLKEAIRD-Z
	X-ITAVALVEAKQARSDIEKLKEAIRD-Z
20	X-QITAVALVEAKQARSDIEKLKEAIRD-Z
	X-AQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-SAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-TSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-ATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-VATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
	X-GVATSAQITAVALVEAKQARSDIEKLKEAIRD-Z
25	X-LGVATSAQITAVALVEAKQARSDIEKLKEAIRD-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (Fmoc) group; a
 30 macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier
 35 group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE XXIII
REPRESENTATIVE DP107/DP178 ANALOG ANTIVIRAL PEPTIDES

Anti-Respiratory syncytial virus peptides

- 5 X-TSVITIELSNIKENKCNCTDAKVKLIKQELDKYKN-Z
X-SVITIELSNIKENKCNCTDAKVKLIKQELDKYKNA-Z
X-VITIELSNIKENKCNCTDAKVKLIKQELDKYKNAV-Z
X-VAVSKVLHLEGEVNKIALLLSTNKAVVSLSNGVS-Z
X-AVSKVLHLEGEVNKIALLLSTNKAVVSLSNGVSV-Z
X-VSKVLHLEGEVNKIALLLSTNKAVVSLSNGVSVL-Z
X-SKVLHLEGEVNKIALLLSTNKAVVSLSNGVSVLT-Z
X-KVLHLEGEVNKIALLLSTNKAVVSLSNGVSVLTS-Z
X-LEGEVNKIALLLSTNKAVVSLSNGVSVLTSKVLD-Z
10 X-GEVNKIALLLSTNKAVVSLSNGVSVLTSKVLDLK-Z
X-EVNKIALLLSTNKAVVSLSNGVSVLTSKVLDLKN-Z
X-VNKIALLLSTNKAVVSLSNGVSVLTSKVLDLKNY-Z
X-NKIALLLSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z
X-KIALLLSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z
X-IALLLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z
X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z
X-VAVSKVLHLEGEVNKIALLLSTNKAVVSLSNGVS-Z
15 X-AVSKVLHLEGEVNKIALLLSTNKAVVSLSNGVSV-Z
X-VSKVLHLEGEVNKIALLLSTNKAVVSLSNGVSVL-Z
X-SKVLHLEGEVNKIALLLSTNKAVVSLSNGVSVLT-Z
X-KVLHLEGEVNKIALLLSTNKAVVSLSNGVSVLTS-Z
X-LEGEVNKIALLLSTNKAVVSLSNGVSVLTSKVLD-Z
X-GEVNKIALLLSTNKAVVSLSNGVSVLTSKVLDLK-Z
X-EVNKIALLLSTNKAVVSLSNGVSVLTSKVLDLKN-Z
X-VNKIALLLSTNKAVVSLSNGVSVLTSKVLDLKNY-Z
20 X-NKIALLLSTNKAVVSLSNGVSVLTSKVLDLKNYI-Z
X-KIALLLSTNKAVVSLSNGVSVLTSKVLDLKNYID-Z
X-IALLLSTNKAVVSLSNGVSVLTSKVLDLKNYIDK-Z
X-ALLSTNKAVVSLSNGVSVLTSKVLDLKNYIDKQ-Z

Anti-human parainfluenza virus 3 peptides

- 25 X-TLNNSVALDPIDISIELNKAQSDLEESKEWIRRSN-Z
X-LNNSVALDPIDISIELNKAQSDLEESKEWIRRSNQ-Z
X-NNSVALDPIDISIELNKAQSDLEESKEWIRRSNQK-Z
X-NSVALDPIDISIELNKAQSDLEESKEWIRRSNQKL-Z
X-SVALDPIDISIELNKAQSDLEESKEWIRRSNQKLD-Z
X-VALDPIDISIELNKAQSDLEESKEWIRRSNQKLDL-Z
X-ALDPIDISIELNKAQSDLEESKEWIRRSNQKLDLDSI-Z
X-LDPIDISIELNKAQSDLEESKEWIRRSNQKLDLDSIG-Z
30 X-DPIDISIELNKAQSDLEESKEWIRRSNQKLDLDSIGN-Z
X-PIDISIELNKAQSDLEESKEWIRRSNQKLDLDSIGNW-Z
X-IDISIELNKAQSDLEESKEWIRRSNQKLDLDSIGNWH-Z
X-DISIELNKAQSDLEESKEWIRRSNQKLDLDSIGNWHQ-Z
X-ISIELNKAQSDLEESKEWIRRSNQKLDLDSIGNWHQS-Z
X-SIELNKAQSDLEESKEWIRRSNQKLDLDSIGNWHQSS-Z
X-IELNKAQSDLEESKEWIRRSNQKLDLDSIGNWHQSST-Z
35 X-ELNKAQSDLEESKEWIRRSNQKLDLDSIGNWHQSSTT-Z
X-TAAVALVEAKQARSQIEKLKEAIRDITNKAVQSVQS-Z

X-AVALVEAKQARSDIEKLKEAIRD TNKAVQSVQSSI-Z
 X-LVEAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNL-Z
 X-VEAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLI-Z
 X-EAKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIV-Z
 X-AKQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVA-Z
 X-KQARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAI-Z
 X-QARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIAIK-Z
 5 X-ARSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIAIKS-Z
 X-RSDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIAIKSV-Z
 X-SDIEKLKEAIRD TNKAVQSVQSSIGNLIVAIAIKSVQ-Z
 X-KLKEAIRD TNKAVQSVQSSIGNLIVAIAIKSVQDYVN-Z
 X-LKEAIRD TNKAVQSVQSSIGNLIVAIAIKSVQDYVNK-Z
 X-AIRD TNKAVQSVQSSIGNLIVAIAIKSVQDYVNKEIV-Z

10 Anti-simian immunodeficiency virus peptides

X-WQEWKVD FLEENITALL EEAQIQQEK NMYELQK-Z
 X-QEWKVD FLEENITALL EEAQIQQEK NMYELQKL-Z
 X-EWKVD FLEENITALL EEAQIQQEK NMYELQKLN-Z
 X-WKVD FLEENITALL EEAQIQQEK NMYELQKLNS-Z
 X-ERKVD FLEENITALL EEAQIQQEK NMYELQKLNSW-Z
 X-RKVD FLEENITALL EEAQIQQEK NMYELQKLNSWD-Z
 15 X-KVD FLEENITALL EEAQIQQEK NMYELQKLNSWDV-Z
 X-VDFLEENITALL EEAQIQQEK NMYELQKLNSWDVF-Z
 X-DFLEENITALL EEAQIQQEK NMYELQKLNSWDVFG-Z
 X-FLEENITALL EEAQIQQEK NMYELQKLNSWDVFGN-Z

Anti-measles virus peptides

20 X-LHRIDL GPPISLERLDVGTNLGN AIAKLEAKELL-Z
 X-HRIDLGPPISLERLDVGTNLGN AIAKLEAKELLE-Z
 X-RIDL GPPISLERLDVGTNLGN AIAKLEAKELLES-Z
 X-IDLGPPISLERLDVGTNLGN AIAKLEAKELLESS-Z
 X-DLGPPISLERLDVGTNLGN AIAKLEAKELLESSD-Z
 X-LGPPISLERLDVGTNLGN AIAKLEAKELLESSDQ-Z
 X-GPPISLERLDVGTNLGN AIAKLEAKELLESSDQI-Z
 25 X-PPISLERLDVGTNLGN AIAKLEAKELLESSDQIL-Z
 X-PISLERLDVGTNLGN AIAKLEAKELLESSDQILR-Z
 X-SLERLDVGTNLGN AIAKLEAKELLESSDQILRSM-Z
 X-LERLDVGTNLGN AIAKLEAKELLESSDQILRSMK-Z

The one letter amino acid code is used.

30 Additionally,
 "X" may represent an amino group, a hydrophobic group,
 including but not limited to carbobenzoxyl, dansyl, or
 T-butyloxycarbonyl; an acetyl group; a 9-
 fluorenylmethoxy-carbonyl (Fmoc) group; a
 macromolecular carrier group including but not limited
 to lipid-fatty acid conjugates, polyethylene glycol,
 or carbohydrates.

35

"Z" may represent a carb xyl group; an amido group; a T-butyloxycarbonyl group; a macr molecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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5.4. SYNTHESIS OF PEPTIDES

The peptides of the invention may be synthesized or prepared by techniques well known in the art. See, for example, Creighton, 1983, *Proteins: Structures and Molecular Principles*, W.H. Freeman and Co., NY, which is incorporated herein by reference in its entirety. Short peptides, for example, can be synthesized on a solid support or in solution. Longer peptides may be made using recombinant DNA techniques. Here, the nucleotide sequences encoding the peptides of the invention may be synthesized, and/or cloned, and expressed according to techniques well known to those of ordinary skill in the art. See, for example, Sambrook, *et al.*, 1989, *Molecular Cloning, A Laboratory Manual*, Vols. 1-3, Cold Spring Harbor Press, NY.

The peptides of the invention may alternatively be synthesized such that one or more of the bonds which link the amino acid residues of the peptides are non-peptide bonds. These alternative non-peptide bonds may be formed by utilizing reactions well known to those in the art, and may include, but are not limited to imino, ester, hydrazide, semicarbazide, and azo bonds, to name but a few. In yet another embodiment of the invention, peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, such that, for example, the stability, bioavailability, and/or inhibitory activity of the peptides is enhanced. For example, hydrophobic groups such as carbobenzoxyl, dansyl, or t-butylloxycarbonyl groups, may be added to the peptides' amino termini. Likewise, an acetyl group or a 9-fluorenylmethoxy-carbonyl group may be placed at the peptides' amino termini. (See "X" in Tables I to IV,

above.) Additionally, the hydrophobic group, t-butyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini. (See "Z" in Tables I to IV, above.)

5 Further, the peptides of the invention may be synthesized such that their steric configuration is altered. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer.

10 Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or inhibitory action of the
15 peptides of the invention.

Any of the peptides described above may, additionally, have a macromolecular carrier group covalently attached to their amino and/or carboxy termini. Such macromolecular carrier groups may
20 include, for example, lipid-fatty acid conjugates, polyethylene glycol, carbohydrates or additional peptides. "X", in Tables I to IV, above, may therefore additionally represent any of the above macromolecular carrier groups covalently attached to
25 the amino terminus of a peptide, with an additional peptide group being preferred. Likewise, "Z", in Tables I to IV, may additionally represent any of the macromolecular carrier groups described above.

30 5.5. ASSAYS FOR ANTI-MEMBRANE FUSION ACTIVITY

Described herein, are methods for ability of a compound, such as the peptides of the invention, to inhibit membrane fusion events. Specifically, assays for cell fusion events are described in Section 5.5.1,

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bel w, and assays for antiviral activity are described in Section 5.5.2, bel w.

5.5.1 ASSAYS FOR CELL FUSION EVENTS

5 Assays for cell fusion events are well known to those of skill in the art, and may be used in conjunction, for example, with the peptides of the invention to test the peptides' antifusogenic capabilities.

10 Cell fusion assays are generally performed in vitro. Such an assay may comprise culturing cells which, in the absence of any treatment would undergo an observable level of syncytial formation. For example, uninfected cells may be incubated in the presence of cells chronically infected with a virus
15 that induces cell fusion. Such viruses may include, but are not limited to, HIV, SIV, or respiratory syncytial virus.

For the assay, cells are incubated in the presence of a peptide to be assayed. For each
20 peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added.

Standard conditions for culturing cells, well known to those of ordinary skill in the art, are used.
25 After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytial formation. Well known stains, such as
30 crystal violet stain, may be used to facilitate the visualization of syncytial formation.

5.5.2 ASSAYS FOR ANTIVIRAL ACTIVITY

The antiviral activity exhibited by the peptides
35 of the invention may be measured, for example, by

asily performed in vitro assays, such as those described below, which can test the peptides' ability to inhibit syncytia formation, or their ability to inhibit infection by cell-free virus. Using these assays, such parameters as the relative antiviral activity of the peptides, exhibit against a given strain of virus and/or the strain specific inhibitory activity of the peptide can be determined.

A cell fusion assay may be utilized to test the peptides' ability to inhibit viral-induced, such as HIV-induced, syncytia formation in vitro. Such an assay may comprise culturing uninfected cells in the presence of cells chronically infected with a syncytial-inducing virus and a peptide to be assayed. For each peptide, a range of peptide concentrations may be tested. This range should include a control culture wherein no peptide has been added. Standard conditions for culturing, well known to those of ordinary skill in the art, are used. After incubation for an appropriate period (24 hours at 37°C, for example) the culture is examined microscopically for the presence of multinucleated giant cells, which are indicative of cell fusion and syncytia formation. Well known stains, such as crystal violet stain, may be used to facilitate syncytial visualization. Taking HIV as an example, such an assay would comprise CD-4⁺ cells (such as Molt or CEM cells, for example) cultured in the presence of chronically HIV-infected cells and a peptide to be assayed.

Other well known characteristics of viral infection may also be assayed to test a peptide's antiviral capabilities. Once again taking HIV as an example, a reverse transcriptase (RT) assay may be utilized to test the peptides' ability to inhibit infection of CD-4⁺ cells by cell-free HIV. Such an assay may compris culturing an appropriate

concentration (i.e., TCID₅₀) of virus and CD-4⁺ cells in the presence of the peptide to be tested. Culture conditions well known to those in the art are used. As above, a range of peptide concentrations may be used, in addition to a control culture wherein no peptide has been added. After incubation for an appropriate period (e.g., 7 days) of culturing, a cell-free supernatant is prepared, using standard procedures, and tested for the presence of RT activity as a measure of successful infection. The RT activity may be tested using standard techniques such as those described by, for example, Goff et al. (Goff, S. et al., 1981, J. Virol. 38:239-248) and/or Willey et al. (Willey, R. et al., 1988, J. Virol. 62:139-147). These references are incorporated herein by reference in their entirety.

Standard methods which are well-known to those of skill in the art may be utilized for assaying non-retroviral activity. See, for example, Pringle et al. (Pringle, C.R. et al., 1985, J. Medical Virology 17:377-386) for a discussion of respiratory syncytial virus and parainfluenza virus activity assay techniques. Further, see, for example, "Zinsser Microbiology", 1988, Joklik, W.K. et al., eds., Appleton & Lange, Norwalk, CT, 19th ed., for a general review of such techniques. These references are incorporated by reference herein in their entirety. In addition, the Examples presented below, in Sections 17, 18, 26 and 27 each provide additional assays for the testing of a compound's antiviral capability.

In vivo assays may also be utilized to test, for example, the antiviral activity of the peptides of the invention. To test for anti-HIV activity, for example, the in vivo model described in Barnett et al. (Barnett, S.W. et al., 1994, Science 266:642-646) may be used.

Additionally, anti-RSV activity can be assayed in vivo via well known mouse models. For example, RSV can be administered intranasally to mice of various inbred strains. Virus replicates in lungs of all strains, but the highest titers are obtained in P/N, C57L/N and DBA/2N mice. Infection of BALB/c mice produces an asymptomatic bronchiolitis characterized by lymphocytic infiltrates and pulmonary virus titers of 10^4 to 10^5 pfu/g of lung tissue (Taylor, G. et al., 1984, Infect. Immun. 43:649-655).

Cotton rat models of RSV are also well known. Virus replicates to high titer in the nose and lungs of the cotton rat but produces few if any signs of inflammation.

5.6. USES OF THE PEPTIDES OF THE INVENTION

The peptides of the invention may be utilized as antifusogenic or antiviral compounds, or as compounds which modulate intracellular processes involving coiled coil peptide structures. Further, such peptides may be used to identify agents which exhibit antifusogenic, antiviral or intracellular modulatory activity. Still further, the peptides of the invention may be utilized as organism or viral type/subtype-specific diagnostic tools.

The antifusogenic capability of the peptides of the invention may additionally be utilized to inhibit or treat/ameliorate symptoms caused by processes involving membrane fusion events. Such events may include, for example, virus transmission via cell-cell fusion, abnormal neurotransmitter exchange via cell-fusion, and sperm-egg fusion. Further, the peptides of the invention may be used to inhibit free viral, such as retroviral, particularly HIV, transmission to uninfected cells wherein such viral infection involves membrane fusion events or involves fusion of a viral

structure with a cell membrane. Among the intracellular disorders involving coiled coil peptides structures which may be ameliorated by the peptides of the invention are disorders involving, for example, bacterial toxins.

5 With respect to antiviral activity, the viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to all strains of the viruses listed above, in Tables V through VII, and IX through XIV.

10 These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and the human T-lymphocyte viruses (HTLV-I and II). The non-human retroviruses whose transmission may be inhibited by the peptides of the invention include, but are not
15 limited to bovine leukosis virus, feline sarcoma and leukemia viruses, simian immunodeficiency, sarcoma and leukemia viruses, and sheep progress pneumonia viruses.

20 Non retroviral viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to human respiratory syncytial virus, canine distemper virus, newcastle disease virus, human parainfluenza virus, influenza viruses, measles viruses, Epstein-Barr viruses, hepatitis B
25 viruses, and simian Mason-Pfizer viruses.

Non enveloped viruses whose transmission may be inhibited by the peptides of the invention include, but are not limited to picornaviruses such as polio viruses, hepatitis A virus, enterovirus, echoviruses
30 and coxsackie viruses, papovaviruses such as papilloma virus, parvoviruses, adenoviruses and reoviruses.

As discussed more fully, below, in Section 5.5.1 and in the Example presented, below, in Section 8, DP107, DP178, DP107 analog and DP178 analog peptides
35 form non-covalent protein-protein interactions which

are required for normal activity of the virus. Thus, the peptides of the invention may also be utilized as components in assays for the identification of compounds that interfere with such protein-protein interactions and may, therefore, act as antiviral agents. These assays are discussed, below, in Section 5.5.1.

As demonstrated in the Example presented below in Section 6, the antiviral activity of the peptides of the invention may show a pronounced type and subtype specificity, i.e., specific peptides may be effective in inhibiting the activity of only specific viruses. This feature of the invention presents many advantages. One such advantage, for example, lies in the field of diagnostics, wherein one can use the antiviral specificity of the peptide of the invention to ascertain the identity of a viral isolate. With respect to HIV, one may easily determine whether a viral isolate consists of an HIV-1 or HIV-2 strain. For example, uninfected CD-4⁺ cells may be co-infected with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, after which the retroviral activity of cell supernatants may be assayed, using, for example, the techniques described above in Section 5.2. Those isolates whose retroviral activity is completely or nearly completely inhibited contain HIV-1. Those isolates whose viral activity is unchanged or only reduced by a small amount, may be considered to not contain HIV-1. Such an isolate may then be treated with one or more of the other DP178 peptides of the invention, and subsequently be tested for its viral activity in order to determine the identity of the viral isolate. The DP107 and DP178 analogs of the invention may also be utilized in a diagnostic capacity specific to the type and subtype of virus or organism in which the specific

peptide sequence is found. A diagnostic procedure as described, above, for DP178, may be used in conjunction with the DP107/DP178 analog of interest.

5.5.1. SCREENING ASSAYS

5 As demonstrated in the Example presented in Section 8, below, DP107 and DP178 portions of the TM protein gp41 form non-covalent protein-protein interactions. As is also demonstrated, the maintenance of such interactions is necessary for
10 normal viral infectivity. Thus, compounds which bind DP107, bind DP178, and/or act to disrupt normal DP107/DP178 protein-protein interactions may act as antifusogenic, antiviral or cellular modulatory agents. Described below are assays for the
15 identification of such compounds. Note that, while, for ease and clarity of discussion, DP107 and DP178 peptides will be used as components of the assays described, but it is to be understood that any of the DP107 analog or DP178 analog peptides described,
20 above, in Sections 5.1 through 5.3 may also be utilized as part of these screens for compounds.

Compounds which may be tested for an ability to bind DP107, DP178, and/or disrupt DP107/DP178 interactions, and which therefore, potentially
25 represent antifusogenic, antiviral or intracellular modulatory compounds, include, but are not limited to, peptides made of D- and/or L-configuration amino acids (in, for example, the form of random peptide libraries; see Lam, K.S. et al., 1991, Nature 354:82-
30 84), phosphopeptides (in, for example, the form of random or partially degenerate, directed phosphopeptide libraries; see, for example, Songyang, Z. et al., 1993, Cell 72:767-778), antibodies, and small organic or inorganic molecules. Synthetic
35 compounds, natural products, and other sources of

potentially effective materials may be screened in a variety of ways, as described in this Section.

The compounds, antibodies, or other molecules identified may be tested, for example, for an ability to inhibit cell fusion or viral activity, utilizing, 5 for example, assays such as those described, above, in Section 5.5.

Among the peptides which may be tested are soluble peptides comprising DP107 and/or DP178 domains, and peptides comprising DP107 and/or DP178 10 domains having one or more mutations within one or both of the domains, such as the M41-P peptide described, below, in the Example presented in Section 8, which contains a isoleucine to proline mutation within the DP178 sequence.

15 In one embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

(a) exposing at least one compound to a peptide comprising a DP107 peptide for a time 20 sufficient to allow binding of the compound to the DP107 peptide;

(b) removing non-bound compounds; and

(c) determining the presence of the compound bound to the DP107 peptide, 25 thereby identifying an agent to be tested for antiviral ability.

In a second embodiment of such screening methods is a method for identifying a compound to be tested for antiviral ability comprising:

30 (a) exposing at least one compound to a peptide comprising a DP178 peptide for a time sufficient to allow binding of the compound to the DP178 peptide;

(b) removing non-bound compounds; and 35

(c) determining the presence of the compound bound to the DP178 peptide, thereby identifying an agent to be tested for antiviral ability.

One method utilizing these types of approaches that may be pursued in the isolation of such DP107-binding or DP178-binding compounds is an assay which would include the attachment of either the DP107 or the DP178 peptide to a solid matrix, such as, for example, agarose or plastic beads, microtiter plate wells, petri dishes, or membranes composed of, for example, nylon or nitrocellulose. In such an assay system, either the DP107 or DP178 protein may be anchored onto a solid surface, and the compound, or test substance, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored component may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the protein and drying.

Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the labeled compound is added to the coated surface containing the anchored DP107 or DP178 peptide. After the reaction is complete, unreacted components are removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the compound is pre-labeled, the detection of label immobilized on the surface indicates that

complexes were formed. Where the labeled component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the compound (the antibody, in turn, may be directly labeled or
5 indirectly labeled with a labeled anti-Ig antibody).

Alternatively, such an assay can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g.,
10 using an immobilized antibody specific for DP107 or DP178, whichever is appropriate for the given assay, or an antibody specific for the compound, i.e., the test substance, in order to anchor any complexes formed in solution, and a labeled antibody specific for the other member of the complex to detect anchored
15 complexes.

By utilizing procedures such as this, large numbers of types of molecules may be simultaneously screened for DP107 or DP178-binding capability, and thus potential antiviral activity.

20 Further, compounds may be screened for an ability to inhibit the formation of or, alternatively, disrupt DP107/DP178 complexes. Such compounds may then be tested for antifusogenic, antiviral or intercellular modulatory capability. For ease of description, DP107
25 and DP178 will be referred to as "binding partners." Compounds that disrupt such interactions may exhibit antiviral activity. Such compounds may include, but are not limited to molecules such as antibodies, peptides, and the like described above.

30 The basic principle of the assay systems used to identify compounds that interfere with the interaction between the DP107 and DP178 peptides involves preparing a reaction mixture containing peptides under conditions and for a time sufficient to allow the two
35 peptides to interact and bind, thus forming a complex.

In order to test a compound for disruptive activity, the reaction is conducted in the presence and absence of the test compound, i.e., the test compound may be initially included in the reaction mixture, or added at a time subsequent to the addition of one of the binding partners; controls are incubated without the test compound or with a placebo. The formation of any complexes between the binding partners is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound indicates that the compound interferes with the interaction of the DP107 and DP178 peptides.

The assay for compounds that interfere with the interaction of the binding partners can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the binding partners. On the other hand, test compounds that disrupt preformed complexes, e.g. compounds with higher binding constants that displace one of the binding partners from the complex, can be tested by adding the test compound to the reaction mixture after complexes have

been formed. The various formats are described briefly below.

In a heterogeneous assay system, one binding partner, e.g., either the DP107 or DP178 peptide, is anchored onto a solid surface, and its binding partner, which is not anchored, is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody specific for the protein may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the binding partner of the immobilized species is added to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the binding partner was pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the binding partner is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the binding partner (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which inhibit complex formation or which disrupt preformed complexes can be detected.

Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one binding partner to anchor any complexes formed in solution, and a labeled antibody specific for the other binding partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds which inhibit complex or which disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the DP107 and DP178 peptides is prepared in which one of the binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the binding partners from the preformed complex will result in the generation of a signal above background. In this way, test substances which disrupt DP-107/DP-178 protein-protein interaction can be identified.

In an alternative screening assay, test compounds may be assayed for their ability to disrupt a DP178/DP107 interaction, as measured immunometrically using an antibody specifically reactive to a DP107/DP178 complex (i.e., an antibody that recognizes neither DP107 nor DP178 individually). Such an assay acts as a competition assay, and is based on techniques well known to those of skill in the art.

The above competition assay may be described, by way of example, and not by way of limitation, by using the DP178 and M41Δ178 peptides and by assaying test

comp unds for the disruption of the c mplexes formed by thes two peptides by immun metrically visualizing DP178/M41Δ178 complexes via the human recombinant Fab, Fab-d, as described, below, in the Example presented in Section 8. M41Δ178 is a maltose binding fusion
5 protein containing a gp41 region having its DP178 domain deleted, and is described, below, in the Example presented in Section 8.

Utilizing such an assay, M41Δ178 may be immobilized onto solid supports such as microtiter
10 wells. A series of dilutions of a test compound may then be added to each M41Δ178-containing well in the presence of a constant concentration of DP-178 peptide. After incubation, at, for example, room
15 temperature for one hour, unbound DP-178 and test compound are removed from the wells and wells are then incubated with the DP178/M41Δ178-specific Fab-d antibody. After incubation and washing, unbound Fab-d
20 is removed from the plates and bound Fab-d is quantitated. A no-inhibitor control should also be conducted. Test compounds showing an ability to
disrupt DP178/M41Δ178 complex formation are identified by their concentration-dependent decrease in the level of Fab-d binding.

A variation of such an assay may be utilized to
25 perform a rapid, high-throughput binding assay which is capable of directly measuring DP178 binding to M41Δ178 for the determination of binding constants of the ligand of inhibitory constants for competitors of DP178 binding.

30 Such an assay takes advantage of accepted radioligand and receptor binding principles. (See, for example, Yamamura, H.I. et al., 1985, "Neurotransmitter Receptor Binding", 2nd ed., Raven Press, NY.) As above, M41Δ178 is immobilized onto a
35 solid support such as a microtiter well. DP178

binding to M41Δ178 is then quantitated by measuring the fraction of DP178 that is bound as ¹²⁵I-DP178 and calculating the total amount bound using a value for specific activity (dpm/μg peptide) determined for each labeled DP178 preparation. Specific binding to
5 M41Δ178 is defined as the difference of the binding of the labeled DP178 preparation in the microtiter wells (totals) and the binding in identical wells containing, in addition, excess unlabeled DP178 (nonspecifics).

10

5.5 PHARMACEUTICAL FORMULATIONS, DOSAGES AND MODES OF ADMINISTRATION

The peptides of the invention may be administered using techniques well known to those in the art.
15 Preferably, agents are formulated and administered systemically. Techniques for formulation and administration may be found in "Remington's Pharmaceutical Sciences", 18th ed., 1990, Mack Publishing Co., Easton, PA. Suitable routes may
20 include oral, rectal, transmucosal, or intestinal administration; parenteral delivery, including intramuscular, subcutaneous, intramedullary injections, as well as, intrathecal, direct intraventricular, intravenous, intraperitoneal,
25 intranasal, or intraocular injections, just to name a few. For injection, the agents of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiological saline
30 buffer. For such transmucosal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In instances wherein intracellular administration
35 of the peptides of the invention or other inhibitory

agents is preferred, techniques well known to those of ordinary skill in the art may be utilized. For example, such agents may be encapsulated into liposomes, then administered as described above. Liposomes are spherical lipid bilayers with aqueous interiors. All molecules present in an aqueous solution at the time of liposome formation are incorporated into the aqueous interior. The liposomal contents are both protected from the external microenvironment and, because liposomes fuse with cell membranes, are effectively delivered into the cell cytoplasm. Additionally, due to their hydrophobicity, when small molecules are to be administered, direct intracellular administration may be achieved.

Nucleotide sequences encoding the peptides of the invention which are to be intracellularly administered may be expressed in cells of interest, using techniques well known to those of skill in the art. For example, expression vectors derived from viruses such as retroviruses, vaccinia viruses, adenovirus-associated viruses, herpes viruses, or bovine papilloma viruses, may be used for delivery and expression of such nucleotide sequences into the targeted cell population. Methods for the construction of such vectors and expression constructs are well known. See, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor NY, and Ausubel et al., 1989, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, NY.

With respect to HIV, peptides of the invention, particularly DP107 and DP178, may be used as therapeutics in the treatment of AIDS. In addition, the peptides may be used as prophylactic measures in previously uninfected individuals after acute exposure

to an HIV virus. Examples of such prophylactic use of these peptides may include, but are not limited to, prevention of virus transmission from mother to infant and other settings where the likelihood of HIV transmission exists, such as, for example, accidents in health care settings wherein workers are exposed to HIV-containing blood products. The successful use of such treatments do not rely upon the generation of a host immune response directed against such peptides.

Effective dosages of the peptides of the invention to be administered may be determined through procedures well known to those in the art which address such parameters as biological half-life, bioavailability, and toxicity. Given the data presented below in Section 6, DP178, for example, may prove efficacious in vivo at doses required to achieve circulating levels of about 1 to about 10 ng per ml of peptide.

A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms or a prolongation of survival in a patient. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD₅₀/ED₅₀. Compounds which exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with

little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (e.g., the concentration of the test compound which achieves a half-maximal inhibition of the fusogenic event, such as a half-maximal inhibition of viral infection relative to the amount of the event in the absence of the test compound) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography (HPLC).

The peptides of the invention may, further, serve the role of a prophylactic vaccine, wherein the host raises antibodies against the peptides of the invention, which then serve to neutralize HIV viruses by, for example, inhibiting further HIV infection.

Administration of the peptides of the invention as a prophylactic vaccine, therefore, would comprise administering to a host a concentration of peptides effective in raising an immune response which is sufficient to neutralize HIV, by, for example, inhibiting HIV ability to infect cells. The exact concentration will depend upon the specific peptide to be administered, but may be determined by using standard techniques for assaying the development of an immune response which are well known to those of ordinary skill in the art. The peptides to be used as vaccines are usually administered intramuscularly.

The peptides may be formulated with a suitable adjuvant in order to enhance the immunological

r sponse. Such adjuvants may include, but are not limited to mineral gels such as aluminum hydr xide; surface active substances such as lysolecithin, pluronic polyols, polyanions; other peptides; oil emulsions; and potentially useful human adjuvants such as BCG and Corynebacterium parvum. Many methods may be used to introduce the vaccine formulations described here. These methods include but are not limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

Alternatively, an effective concentration of polyclonal or monoclonal antibodies raised against the peptides of the invention may be administered to a host so that no uninfected cells become infected by HIV. The exact concentration of such antibodies will vary according to each specific antibody preparation, but may be determined using standard techniques well known to those of ordinary skill in the art. Administration of the antibodies may be accomplished using a variety of techniques, including, but not limited to those described in this section.

For all such treatments described above, the exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition. (See e.g. Fingl et al., 1975, in "The Pharmacological Basis of Therapeutics", Ch. 1 p1).

It should be noted that the attending physician would know how to and when to terminate, interrupt, or adjust administration due to toxicity, or to organ dysfunctions. Conversely, the attending physician would also know to adjust treatment to higher levels if the clinical response were not adequate (precluding toxicity). The magnitude of an administered dose in the management of the oncogenic disorder of interest

will vary with the severity of the condition to be treated and the route of administration. The dose and perhaps dose frequency, will also vary according to the age, body weight, and response of the individual patient. A program comparable to that discussed above
5 may be used in veterinary medicine.

Use of pharmaceutically acceptable carriers to formulate the compounds herein disclosed for the practice of the invention into dosages suitable for systemic administration is within the scope of the
10 invention. With proper choice of carrier and suitable manufacturing practice, the compositions of the present invention, in particular, those formulated as solutions, may be administered parenterally, such as by intravenous injection. The compounds can be
15 formulated readily using pharmaceutically acceptable carriers well known in the art into dosages suitable for oral administration. Such carriers enable the compounds of the invention to be formulated as tablets, pills, capsules, liquids, gels, syrups,
20 slurries, suspensions and the like, for oral ingestion by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective
25 amount to achieve its intended purpose. Determination of the effective amounts is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein.

In addition to the active ingredients, these
30 pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated
35

for oral administration may be in the form of tablets, dragees, capsules, or solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are, in particular, fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; cellulose preparations such as, for example, maize starch, wheat starch, rice starch, potato starch, gelatin, gum tragacanth, methyl cellulose, hydroxypropylmethyl-cellulose, sodium carboxymethylcellulose, and/or polyvinylpyrrolidone (PVP). If desired, disintegrating agents may be

add d, such as the cross-linked polyvinyl pyrrolidone, agar, or alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings. For this purpose, concentrated sugar solutions may be used, which may optionally contain gum arabic, talc, polyvinyl pyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for identification or to characterize different combinations of active compound doses.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a plasticizer, such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients in admixture with filler such as lactose, binders such as starches, and/or lubricants such as talc or magnesium stearate and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycols. In addition, stabilizers may be added.

6. EXAMPLE: DP178 (SEQ ID:1) IS A POTENT INHIBITOR OF HIV-1 INFECTION

In this example, DP178 (SEQ ID:1) is shown to be a potent inhibitor of HIV-1 mediated CD-4⁺ cell-cell fusion and infection by cell free virus. In the fusion assay, this peptide completely blocks virus induced syncytia formation at concentrations of from 1-10 ng/ml. In the infectivity assay the inhibitory concentration is somewhat higher, blocking infection at 90ng/ml. It is further shown that DP178 (SEQ ID:1) shows that the antiviral activity of DP178 (SEQ ID:1)

is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), representing a HIV-1-derived DP178 homolog is also found to block HIV-1-mediated syncytia formation.

5

6.1. MATERIALS AND METHODS

6.1.1. PEPTIDE SYNTHESIS

Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A peptide synthesizer. Generally, unless otherwise noted, the peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides were prepared using Rink resin (Advanced Chemtech) while peptides containing free carboxy termini were synthesized on Wang (p-alkoxy-benzyl-alcohol) resin (Bachem). First residues were double coupled to the appropriate resin and subsequent residues were single coupled. Each coupling step was followed by acetic anhydride capping. Peptides were cleaved from the resin by treatment with trifluoroacetic acid (TFA) (10ml), H₂O (0.5ml), thioanisole (0.5ml), ethanedithiol (0.25ml), and crystalline phenol (0.75g). Purification was carried out by reverse phase HPLC. Approximately 50mg samples of crude peptide were chromatographed on a Waters Delta Pak C18 column (19mm x 30cm, 15 μ spherical) with a linear gradient; H₂O/acetonitrile 0.1% TFA. Lyophilized peptides were stored desiccated and peptide solutions were made in water at about 1mg/ml. Electrospray mass spectrometry yielded the following results: DP178 (SEQ ID:1):4491.87 (calculated 4491.94); DP-180 (SEQ ID:2):4491.45 (calculated 4491.94); DP-185 (SEQ ID:3):not done (calculated 4546.97).

35

6.1.2. VIRUS

The HIV-1_{LAI} virus was obtained from R. Gallo (Popovic, M. et al., 1984, Science 224:497-508) and propagated in CEM cells cultured in RPMI 1640 containing 10% fetal calf serum. Supernatant from the infected CEM cells was passed through a 0.2µm filter and the infectious titer estimated in a microinfectivity assay using the AA5 cell line to support virus replication. For this purpose, 25µl of serial diluted virus was added to 75µl AA5 cells at a concentration of 2×10^5 /ml in a 96-well microtitre plate. Each virus dilution was tested in triplicate. Cells were cultured for eight days by addition of fresh medium every other day. On day 8 post infection, supernatant samples were tested for virus replication as evidenced by reverse transcriptase activity released to the supernatant. The TCID₅₀ was calculated according to the Reed and Muench formula (Reed, L.J. et al., 1938, Am. J. Hyg. 27:493-497). The titer of the HIV-1_{LAI} and HIV-1_{MN} stocks used for these studies, as measured on the AA5 cell line, was approximately 1.4×10^6 and 3.8×10^4 TCID₅₀/ml, respectively.

6.1.3. CELL FUSION ASSAY

Approximately 7×10^4 Molt cells were incubated with 1×10^4 CEM cells chronically infected with the HIV-1_{LAI} virus in 96-well plates (one-half area cluster plates; Costar, Cambridge, MA) in a final volume of 100µl culture medium as previously described (Matthews, T.J. et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5428). Peptide inhibitors were added in a volume of 10µl and the cell mixtures were incubated for 24 hr. at 37°C. At that time, multinucleated giant cells were estimated by microscopic examination

at a 40x magnification which allowed visualization of the entire well in a single field.

6.1.4. CELL FREE VIRUS INFECTION ASSAY

Synthetic peptides were incubated at 37°C with
5 either 247 TCID₅₀ (for experiment depicted in FIG. 2),
or 62 TCID₅₀ (for experiment depicted in FIG.3) units
of HIV-1_{LAI} virus or 25 TCID₅₀ units of HIV-2_{MBZ} and CEM
CD4⁺ cells at peptide concentrations of 0, 0.04, 0.4,
10 4.0, and 40µg/ml for 7 days. The resulting reverse
transcriptase (RT) activity in counts per minute was
determined using the assay described, below, in
Section 6.1.5. See, Reed, L.J. et al., 1938, Am. J.
Hyg. 27: 493-497 for an explanation of TCID₅₀
calculations.

15

6.1.5. REVERSE TRANSCRIPTASE ASSAY

The micro-reverse transcriptase (RT) assay was
adapted from Goff et al. (Goff, S. et al., 1981, J.
Virol. 38:239-248) and Willey et al. (Willey, R. et
20 al., 1988, J. Virol. 62:139-147). Supernatants from
virus/cell cultures are adjusted to 1% Triton-X100. A
10µl sample of supernatant was added to 50µl of RT
cocktail in a 96-well U-bottom microtitre plate and
the samples incubated at 37°C for 90 min. The RT
25 cocktail contained 75mM KCl, 2mM dithiothreitol, 5mM
MgCl₂, 5µg/ml poly A (Pharmacia, cat. No. 27-4110-01),
0.25 units/ml oligo dT (Pharmacia, cat. No. 27-7858-
01), 0.05% NP40, 50mM Tris-HCl, pH 7.8, 0.5µM non-
radioactive dTTP, and 10µCi/ml ³²P-dTTP (Amersham, cat.
30 No. PB.10167).

After the incubation period, 40µl of reaction
mixture was applied to a Schleicher and Schuell (S+S)
NA45 membrane (or DE81 paper) saturated in 2 x SSC
buffer (0.3M NaCl and 0.003M sodium citrate) held in a
35 S+S Minifold over one sheet of GB003 (S+S) filter

paper, with partial vacuum applied. Each well of the minifold was washed four times with 200 μ l 2xSSC, under full vacuum. The membrane was removed from the minifold and washed 2 more times in a pyrex dish with an excess of 2xSSC. Finally, the membrane was drained
5 on absorbent paper, placed on Whatman #3 paper, covered with Saran wrap, and exposed to film overnight at -70°C.

6.2. RESULTS

10 6.2.1. PEPTIDE INHIBITION OF INFECTED CELL-INDUCED SYNCYTIA FORMATION

The initial screen for antiviral activity assayed peptides' ability to block syncytium formation induced by overnight co-cultivation of uninfected Molt4 cells
15 with chronically HIV-1 infected CEM cells. The results of several such experiments are presented herein. In the first of these experiments, serial DP178 (SEQ ID:1) peptide concentrations between 10 μ g/ml and 12.5ng/ml were tested for blockade of the
20 cell fusion process. For these experiments, CEM cells chronically infected with either HIV-1_{LA1}, HIV-1_{MAN}, HIV-1_{RF}, or HIV-1_{SF2} virus were cocultivated overnight with uninfected Molt 4 cells. The results (FIG. 4) show that DP178 (SEQ ID:1) afforded complete protection
25 against each of the HIV-1 isolates down to the lowest concentration of DP178 (SEQ ID:1) used. For HIV_{LA1} inhibition, the lowest concentration tested was 12.5ng/ml; for all other HIV-1 viruses, the lowest concentration of DP178 (SEQ ID:1) used in this study
30 was 100ng/ml. A second peptide, DP-180 (SEQ ID:2), containing the same amino acid residues as DP178 (SEQ ID:1) but arranged in a random order exhibited no evidence of anti-fusogenic activity even at the high concentration of 40 μ g/ml (FIG. 4). These observations
35 indicate that the inhibitory effect of DP178 (SEQ

ID:1) is primary sequence-specific and not related to non-specific peptid /protein interactions. The actual endpoint (i.e., the lowest effective inhibitory concentration) of DP178 inhibitory action is within the range of 1-10 ng/ml.

5 The next series of experiments involved the preparation and testing of a DP178 (SEQ ID:1) homolog for its ability to inhibit HIV-1-induced syncytia formation. As shown in FIG. 1, the sequence of DP-185 (SEQ ID:3) is slightly different from DP178 (SEQ ID:1) in that its primary sequence is taken from the HIV-1_{SP2} isolate and contains several amino acid differences relative to DP178 (SEQ ID:1) near the N terminus. As shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the lowest concentration tested.

10 The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP178 (SEQ ID:1) blocked HIV-1-mediated syncytia formation at peptide concentrations below 1ng/ml. DP178 (SEQ ID:1) failed, however, to block HIV-2 mediated syncytia formation at concentrations as high as 10µg/ml. This striking 4 log selectivity of DP178 (SEQ ID:1) as an inhibitor of HIV-1-mediated cell fusion demonstrates an unexpected HIV-1 specificity in the action of DP178 (SEQ ID:1). DP178 (SEQ ID:1) inhibition of HIV-1-mediated cell fusion, but the peptide's inability to inhibit HIV-2 mediated cell fusion in the same cell type at the concentrations tested provides further evidence for the high degree of selectivity associated with the antiviral action of DP178 (SEQ ID:1).

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6.2.2. PEPTIDE INHIBITION OF INFECTION BY CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested for its ability to block CD-4⁺ CEM cell infection by cell free HIV-1 virus. The results, shown in FIG. 2, are from an experiment in which DP178 (SEQ ID:1) was assayed for its ability to block infection of CEM cells by an HIV-1_{LAI} isolate. Included in the experiment were three control peptides, DP-116 (SEQ ID:9), DP-125 (SEQ ID:8), and DP-118 (SEQ ID:10). DP-116 (SEQ ID:9) represents a peptide previously shown to be inactive using this assay, and DP-125 (SEQ ID:8; Wild, C. *et al.*, 1992, Proc. Natl. Acad. Sci. USA 89:10,537) and DP-118 (SEQ ID:10) are peptides which have previously been shown to be active in this assay. Each concentration (0, 0.04, 0.4, 4, and 40 µg/ml) of peptide was incubated with 247 TCID₅₀ units of HIV-1_{LAI} virus and CEM cells. After 7 days of culture, cell-free supernatant was tested for the presence of RT activity as a measure of successful infection. The results, shown in FIG. 2, demonstrate that DP178 (SEQ ID:1) inhibited the de novo infection process mediated by the HIV-1 viral isolate at concentrations as low as 90ng/ml (IC₅₀=90ng/ml). In contrast, the two positive control peptides, DP-125 (SEQ ID:8) and DP-118 (SEQ ID:10), had over 60-fold higher IC₅₀ concentrations of approximately 5 µg/ml.

In a separate experiment, the HIV-1 and HIV-2 inhibitory action of DP178 (SEQ ID:1) was tested with CEM cells and either HIV-1_{LAI} or HIV-2_{NIH2}. 62 TCID₅₀ HIV-1_{LAI} or 25 GCID₅₀ HIV-2_{NIH2} were used in these experiments, and were incubated for 7 days. As may be seen in FIG. 3, DP178 (SEQ ID:1) inhibited HIV-1 infection with an IC₅₀ of about 31ng/ml. In contrast, DP178 (SEQ ID:1) exhibited a much higher IC₅₀ for HIV-2_{NIH2}, thus making DP178 (SEQ ID:1) two logs more potent

as a HIV-1 inhibitor than a HIV-2 inhibitor. This finding is consistent with the results of the fusion inhibition assays described, above, in Section 6.2.1, and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

5

7. EXAMPLE: THE HIV-1 INHIBITOR, DP178 (SEQ ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthetic peptide inhibitor DP178 (SEQ ID:1) is shown to be non-cytotoxic to cells in culture, even at the highest peptide concentrations (40µg/ml) tested.

10

7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

Approximately 3.8×10^5 CEM cells for each peptide concentration were incubated for 3 days at 37°C in T25 flasks. Peptides tested were DP178 (SEQ ID:1) and DP-116 (SEQ ID:9), as described in FIG. 1. Peptides were synthesized as described, above, in Section 6.1. The concentrations of each peptide used were 0, 2.5, 10, and 40µg/ml. Cell counts were taken at incubation times of 0, 24, 48, and 72 hours.

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7.2. RESULTS

Whether the potent HIV-1 inhibitor DP178 (SEQ ID:1) exhibited any cytotoxic effects was assessed by assaying the peptide's effects on the proliferation and viability of cells in culture. CEM cells were incubated in the presence of varying concentrations of DP178 (SEQ ID:1), and DP-116 (SEQ ID:9), a peptide previously shown to be ineffective as a HIV inhibitor (Wild, C. et al., 1992, Proc. Natl. Acad. Sci. USA 89:10,537-10,541). Additionally, cells were incubated in the absence of either peptide.

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The results of the cytotoxicity study demonstrate that DP178 (SEQ ID:1) exhibits no cytotoxic effects on cells in culture. As can be seen, below, in Table XXIV, even the proliferation and viability characteristics of cells cultured for 3 days in the presence of the highest concentration of DP178 (SEQ ID:1) tested (40 μ g/ml) do not significantly differ from the DP-116 (SEQ ID:9) or the no-peptide controls. The cell proliferation data is also represented in graphic form in FIG. 6. As was demonstrated in the Working Example presented above in Section 6, DP178 (SEQ ID:1) completely inhibits HIV-1 mediated syncytia formation at peptide concentrations between 1 and 10ng/ml, and completely inhibits cell-free viral infection at concentrations of at least 90ng/ml. Thus, this study demonstrates that even at peptide concentrations greater than 3 log higher than the HIV inhibitory dose, DP178 (SEQ ID:1) exhibits no cytotoxic effects.

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TABLE XXIV

5	Peptide	Peptide Concentration $\mu\text{g/ml}$	% Viability at time (hours)			
			0	24	48	72
10	DP178 (SEQ ID:1)	40	98	97	95	97
		10	98	97	98	98
		2.5	98	93	96	96
15	DP116 (SEQ ID:9)	40	98	95	98	97
		10	98	95	93	98
		2.5	98	96	98	99
20	No Peptide	0	98	97	99	98

8. EXAMPLE: THE INTERACTION OF DP178 AND DP107

Soluble recombinant forms of gp41 used in the
 example described below provide evidence that the
 DP178 peptide associates with a distal site on gp41
 whose interactive structure is influenced by the DP107
 leucine zipper motif. A single mutation disrupting
 the coiled-coil structure of the leucine zipper domain
 transformed the soluble recombinant gp41 protein from
 an inactive to an active inhibitor of HIV-1 fusion.
 This transformation may result from liberation of the
 potent DP178 domain from a molecular clasp with the
 leucine zipper, DP107, determinant. The results also
 indicate that the anti-HIV activity of various gp41
 derivatives (peptides and recombinant proteins) may be

due to their ability to form complexes with viral gp41 and interfere with its fusogenic process.

8.1. MATERIALS AND METHODS

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8.1.1. CONSTRUCTION OF FUSION PROTEINS AND GP41 MUTANTS

Construction of fusion proteins and mutants shown in FIG. 7 was accomplished as follows: the DNA sequence corresponding to the extracellular domain of gp41 (540-686) was cloned into the Xmn I site of the expression vector pMal-p2 (New England Biolab) to give M41. The gp41 sequence was amplified from pgtat (Malim et al., 1988, Nature 355: 181-183) by using polymerase chain reaction (PCR) with upstream primer 15 5'-ATGACGCTGACGGTACAGGCC-3' (primer A) and downstream primer 5'-TGACTAAGCTTAATACCACAGCCAATTTGTTAT-3' (primer B). M41-P was constructed by using the T7-Gen in vitro mutagenesis kit from United States Biochemicals (USB) following the supplier's 20 instructions. The mutagenic primer (5'-GGAGCTGCTTGGGGCCCCAGAC-3') introduces an Ile to Pro mutation in M41 at position 578. M41Δ107, from which the DP-107 region has been deleted, was made using a deletion mutagenic primer 5'- 25 CCAAATCCCCAGGAGCTGCTCGAGCTGCACTATACCAGAC-3' (primer C) following the USB T7-Gen mutagenesis protocol. M41Δ178, from which the DP-178 region has been deleted, was made by cloning the DNA fragment corresponding to gp41 amino acids 540-642 into the 30 Xmn I site of pMal-p2. Primer A and 5'-ATAGCTTCTAGATTAAATTGTTAATTTCTCTGTCCC-3' (primer D) were used in the PCR with the template pgtat to generate the inserted DNA fragments. M41-P was used as the template with primer A and D in PCR to generate M41- 35 PA178. All inserted sequences and mutated residues

wer checked by restriction enzyme analysis and confirmed by DNA sequencing.

8.1.2. PURIFICATION AND CHARACTERIZATION OF FUSION PROTEINS

5 The fusion proteins were purified according to the protocol described in the manufacturer's brochure of protein fusion and purification systems from New England Biolabs (NEB). Fusion proteins (10 ng) were analyzed by electrophoresis on 8% SDS polyacrylamide
10 gels. Western blotting analysis was performed as described by Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. 18, pp. 64-75. An HIV-1 positive serum diluted 1000-fold,
15 or a human Fab derived from repertoire cloning was used to react with the fusion proteins. The second antibody was HRP-conjugated goat antihuman Fab. An ECL Western blotting detection system (Amersham) was used to detect the bound antibody. A detailed
20 protocol for this detection system was provided by the manufacturer. Rainbow molecular weight markers (Amersham) were used to estimate the size of fusion proteins.

25 8.1.3. CELL FUSION ASSAYS FOR ANTI-HIV ACTIVITY

 Cell fusion assays were performed as previously described (Matthews et al., 1987, Proc. Natl. Acad. Sci. USA 84: 5424-5481). CEM cells (7×10^4) were incubated with HIV-1_{MB} chronically infected CEM cells
30 (10^4) in 96-well flat-bottomed half-area plates (Costar) in 100 μ l culture medium. Peptide and fusion proteins at various concentrations in 10 μ l culture medium were incubated with the cell mixtures at 37°C for 24 hours. Multinucleated syncytia were estimated
35 with microscopic examination. Both M41 and M41-P did

n t sh w cytotoxicity at the concentrations tested and shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell fusion activity was carried out in the presence of 10 nM DP178 and various concentrations of M41Δ178 or M41-PA178 as indicated in FIG. 9. There was no observable syncytia in the presence of 10 nM DP178. No peptide or fusion protein was added in the control samples.

8.1.4. ELISA ANALYSIS OF DP178 BINDING TO THE LEUCINE ZIPPER MOTIF OF GP41

The amino acid sequence of DP178 used is: YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. For enzyme linked immunoassay (ELISA), M41Δ178 or M41-PA178 (5 μg/ml) in 0.1M NaHCO₃, pH 8.6, were coated on 96 wells Linbro ELISA plates (Flow Lab, Inc.) overnight. Each well was washed three times with distilled water then blocked with 3% bovine serum albumin (BSA) for 2 hours. After blocking, peptides with 0.5% BSA in TBST (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% Tween 20) were added to the ELISA plates and incubated at room temperature for 1 hour. After washing three times with TBST, Fab-d was added at a concentration of 10 ng/ml with 0.5% BSA in TBST. The plates were washed three times with TBST after incubation at room temperature for 1 hour. Horse radish peroxidase (HRP) conjugated goat antihuman Fab antiserum at a 2000 fold dilution in TBST with 0.5% BSA was added to each well and incubated at room temperature for 45 minutes. The plates were then washed four times with TBST. The peroxidase substrate o-phenylene diamine (2.5 mg/ml) and 0.15% H₂O₂ were added to develop the color. The reaction was stopped with an equal volume of 4.5 N H₂SO₄ after incubation at room temperature for 10 minutes. The optical density of the stopped reaction mixture was measured with a micro plate reader

(Molecular Design) at 490 nm. Results are shown in FIG. 10.

8.2. RESULTS

8.2.1. THE EXPRESSION AND CHARACTERIZATION OF THE ECTODOMAIN OF gp41

5 As a step toward understanding the roles of the two helical regions in gp41 structure and function, the ectodomain of gp41 was expressed as a maltose binding fusion protein (M41) (FIG. 7). The fusogenic
10 peptide sequence at the N-terminal of gp41 was omitted from this recombinant protein and its derivatives to improve solubility. The maltose binding protein facilitated purification of the fusion proteins under relatively mild, non-denaturing conditions. Because
15 the M41 soluble recombinant gp41 was not glycosylated, lacked several regions of the transmembrane protein (*i.e.*, the fusion peptide, the membrane spanning, and the cytoplasmic domains), and was expressed in the absence of gp120, it was not expected to precisely
20 reflect the structure of native gp41 on HIV-1 virions. Nevertheless, purified M41 folded in a manner that preserved certain discontinuous epitopes as evidenced by reactivity with human monoclonal antibodies, 98-6, 126-6, and 50-69, previously shown to bind
25 conformational epitopes on native gp41 expressed in eukaryotic cells (Xu et al., 1991, J. Virol. 65: 4832-4838; Chen, 1994, J. Virol. 68:2002-2010). Thus, at least certain regions of native gp41 defined by these antibodies appear to be reproduced in the recombinant
30 fusion protein M41. Furthermore, M41 reacted with a human recombinant Fab (Fab-d) that recognizes a conformational epitope on gp41 and binds HIV-1 virions as well as HIV-1 infected cells but not uninfected cells as analyzed by FACS. Deletion of either helix
35 motif, *i.e.*, DP107 or DP178, of the M41 fusion protein

eliminated reactivity with Fab-d. These results indicate that both helical regions, separated by 60 amino acids in the primary sequence, are required to maintain the Fab-d epitope.

5

8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF GP41

The wild type M41 fusion protein was tested for anti-HIV-1 activity. As explained, *supra*, synthetic
10 peptides corresponding to the leucine zipper (DP107) and the C-terminal putative helix (DP178) show potent anti-HIV activity. Despite inclusion of both these regions, the recombinant M41 protein did not affect HIV-1 induced membrane fusion at concentrations as
15 high as 50 μ M (Table XXV, below).

TABLE XXV
DISRUPTION OF THE LEUCINE ZIPPER OF
GP41 FREES THE ANTI-HIV MOTIF

20		<u>DP107</u>	<u>DP178</u>	<u>M41</u>	<u>M41-P</u>	<u>M41-PA178</u>
	Cell fusion (IC ₅₀)	1 μ M	1 nM	> 50 μ M	83 nM	> 50 μ M
25	Fab-D binding (K _D)	-	-	3.5x10 ⁻⁹	2.5x10 ⁻⁸	-
	HIV infectiv- ity (IC ₅₀)	1 μ M	80 nM	> 16 μ M	66 nM	> 8 μ M

30

1 The affinity constants of Fab-d binding to the fusion proteins were determined using a protocol described by B. Friguet et al., 1985, J. Immunol. Method. 77:305-319.

- = No detectable binding of Fab-d to the fusion proteins.

35

Antiviral Infectivity Assays. 20 μ l of serially diluted virus stock was incubated for 60 minutes at ambient temperature with 20 μ l of the indicated

concentration of purified recombinant fusion protein in RPMI 1640 containing 10% fetal bovine serum and antibiotics in a 96-well microtiter plate. 20 μ l of CEM4 cells at 6×10^5 cells/ml were added to each well, and cultures were incubated at 37°C in a humidified CO₂ incubator. Cells were cultured for 9 days by the addition of fresh medium every 2 to 3 days. On days 5, 7, and 9 postinfection, supernatant samples were assayed for reverse transcriptase (RT) activity, as described below, to monitor viral replication. The 50% tissue culture infectious dose (TCID₅₀) was calculated for each condition according to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-497. RT activity was determined by a modification of the published methods of Goff et al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. 62:139-147 as described in Chen et al., 1993, AIDS Res. Human Retroviruses 9:1079-1086.

10

Surprisingly, a single amino acid substitution, proline in place of isoleucine in the middle of the leucine zipper motif, yielded a fusion protein (M41-P) which did exhibit antiviral activity (Table XXV and Fig. 8). As seen in Table XXV, M41-P blocked syncytia formation by 90% at approximately 85 nM and neutralized HIV-1_{MB} infection by 90% at approximately 70 nM concentrations. The anti-HIV-1 activity of M41-P appeared to be mediated by the C-terminal helical sequence since deletion of that region from M41-P yielded an inactive fusion protein, M41-PA178 (Table XXV). This interpretation was reinforced by experiments demonstrating that a truncated fusion protein lacking the DP178 sequence, M41 Δ 178, abrogated the potent anti-fusion activity of the DP178 peptide in a concentration-dependent manner (FIG. 9). The same truncated fusion protein containing the proline mutation disrupting the leucine zipper, M41-PA178, was not active in similar competition experiments (FIG. 9). The results indicate that the DP178 peptide associates with a second site on gp41 whose interactive structure is dependent on a wild type leucine zipper sequence. A similar interaction may occur within the wild type fusion protein, M41, and act to form an intramolecular clasp which sequesters

35

th DP178 region, making it unavailable for anti-viral activity.

A specific association between these two domains is also indicated by other human monoclonal Fab-d studies. For example, Fab-d failed to bind either the DP178 peptide or the fusion protein M41Δ178, but its epitope was reconstituted by simply mixing these two reagents together (FIG. 10). Again, the proline mutation in the leucine zipper domain of the fusion protein, M41-PA178, failed to reconstitute the epitope in similar mixing experiments.

9. EXAMPLE: METHOD FOR COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES

A number of known coiled-coil sequences have been well described in the literature and contain heptad repeat positioning for each amino acid. Coiled-coil nomenclature labels each of seven amino acids of a heptad repeat A through G, with amino acids A and D tending to be hydrophobic positions. Amino acids E and G tend to be charged. These four positions (A, D, E, and G) form the amphipathic backbone structure of a monomeric alpha-helix. The backbones of two or more amphipathic helices interact with each other to form di-, tri-, tetrameric, etc., coiled-coil structures. In order to begin to design computer search motifs, a series of well characterized coiled coils were chosen including yeast transcription factor GCN4, Influenza Virus hemagglutinin loop 36, and human proto-oncogenes c-Myc, c-Fos, and c-Jun. For each peptide sequence, a strict homology for the A and D positions, and a list of the amino acids which could be excluded for the B, C, E, F, and G positions (because they are not observed in these positions) was determined. Motifs were tailored to the DP107 and DP178 sequences by

deducing the most likely possibilities for heptad positioning of the amino acids of HIV-1 Bru DP-107, which is known to have coiled-coil structure, and HIV-1 Bru DP178, which is still structurally undefined. The analysis of each of the sequences is contained in
 5 FIG. 12. For example, the motif for GCN4 was designed as follows:

1. The only amino acids (using standard single letter amino acid codes) found in the A or D positions of GCN4 were [LMNV].
- 10 2. All amino acids were found at B, C, E, F, and G positions except {CFGIMPTW}.
3. The PESEARCH motif would, therefore, be written as follows:
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-
 15 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-
 [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)

Translating or reading the motif: "at the first A
 20 position either L, M, N, or V must occur; at positions B and C (the next two positions) accept everything except C, F, G, I, M, P, T, or W; at the D position either L, M, N, or V must occur; at positions E, F, and G (the next 3 positions) accept everything except
 25 C, F, G, I, M, P, T, or W." This statement is contained four times in a 28-mer motif and five times in a 35-mer motif. The basic motif key then would be: [LMNV]-{CFGIMPTW}. The motif keys for the remaining well described coiled-coil sequences are summarized in
 30 FIG. 12.

The motif design for DP107 and DP178 was slightly different than the 28-mer model sequences described above due to the fact that heptad repeat positions are not defined and the peptides are both longer than 28
 35 residues. FIG. 13 illustrates several possible

sequence alignments for both DP107 and DP178 and also includes motif designs based on 28-mer, 35-mer, and full-length peptides. Notice that only slight differences occur in the motifs as the peptides are lengthened. Generally, lengthening the base peptide results in a less stringent motif. This is very useful in broadening the possibilities for identifying DP107-or DP-178-like primary amino acid sequences referred to in this document as "hits".

In addition to making highly specific motifs for each type peptide sequence to be searched, it is also possible to make "hybrid" motifs. These motifs are made by "crossing" two or more very stringent motifs to make a new search algorithm which will find not only both "parent" motif sequences but also any peptide sequences which have similarities to one, the other, or both "parents". For example, in FIG. 14 the "parent" sequence of GCN4 is crossed with each of the possible "parent" motifs of DP-107. Now the hybrid motif must contain all of the amino acids found in the A and D positions of both parents, and exclude all of the amino acids not found in either parent at the other positions. The resulting hybrid from crossing GCN4 or [LMNV]{CFGIMPTW} and DP107 (28-mer with the first L in the D position) or [ILQT]{CDFIMPST}, is [ILMNQTV]{CFIMPT}. Notice that now only two basic hybrid motifs exist which cover both framing possibilities, as well as all peptide lengths of the parent DP-107 molecule. FIG. 15 represents the "hybridizations" of GCN4 with DP-178. FIG. 16 represents the "hybridizations" of DP107 and DP178. It is important to keep in mind that the represented motifs, both parent and hybrid, are motif keys and not the depiction of the full-length motif needed to actually do the computer search.

Hybridizations can be performed in any combination of two or more motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 (also both frames). Notice that the resulting motifs are now becoming much more similar to each other. In fact, the first and third hybrid motifs are actually subsets of the second and fourth hybrid motifs respectively. This means that the first and third hybrid motifs are slightly more stringent than the second and fourth. It should also be noted that with only minor changes in these four motifs, or by hybridizing them, a single motif could be obtained which would find all of the sequences. However, it should be remembered that stringency is also reduced. Finally, the most broad-spectrum and least-stringent hybrid motif is described in FIG. 18 which summarizes the hybridization of GCN4, DP107 (both frames), DP178 (both frames), c-Fos, c-Jun, c-Myc, and Flu loop 36.

A special set of motifs was designed based on the fact that DP-178 is located only approximately ten amino acids upstream of the transmembrane spanning region of gp41 and just C-terminal to a proline which separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when membrane associated, and that the proline might aid in the initiation of the helix formation. The same arrangement was observed in Respiratory Syncytial Virus; however, the DP178-like region in this virus also had a leucine zipper just C-terminal to the proline. Therefore, N-terminal proline-leucine zipper motifs were designed to analyze whether any other viruses might contain this same pattern. The motifs are summarized in FIG. 19.

The PC/Gene protein database contains 5879 viral amino acid sequences (library file PVIRUSES; CD-ROM

release 11.0). Of these, 1092 are viral enveloped r glycoprotein in sequences (library file PVIRUSE1). Tables V through XIV contain lists of protein names and motif hit locations for all the motifs searched.

5

10. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION
OF DP107 AND DP178-LIKE SEQUENCES
IN HUMAN IMMUNODEFICIENCY VIRUS**

FIG. 20 represents search results for HIV-1 BRU isolate gp41 (PC/Gene protein sequence PENV_HV1BR). Notice that the hybrid motif which crosses DP-107 and DP-178 (named 107x178x4; the same motif as found in FIG. 16 found three hits including amino acids 550-599, 636-688, and 796-823. These areas include DP-107 plus eight N-terminal and four C-terminal amino acids; DP178 plus seven N-terminal and ten C-terminal amino acids; and an area inside the transmembrane region (cytoplasmic). FIG. 20 also contains the results obtained from searching with the motif named ALLMOTI5, for which the key is found in FIG. 17 ({CDGHP}{CFP}x5). This motif also found three hits including DP107 (amino acids 510-599), DP178 (615-717), and a cytoplasmic region (772-841). These hits overlap the hits found by the motif 107x178x4 with considerable additional sequences on both the amino and carboxy termini. This is not surprising in that 107x178x4 is a subset of the ALLMOTI5 hybrid motif. Importantly, even though the stringency of ALLMOTI5 is considerably less than 107x178x4, it still selectively identifies the DP107 and DP178 regions of gp41 shown to contain sequences for inhibitory peptides of HIV-1. The results of these two motif searches are summarized in Table V under the PC/Gene protein sequence name PENV_HV1BR. The proline-leucine zipper motifs also gave several hits in HIV-1 BRU including 503-525 which is

at the very C-terminal of gp120, just upstream of the
 cleavage site (P7LZIPC and P12LZIPC); and 735-768 in
 the cytoplasmic domain of gp41 (P23LZIPC). These
 results are found in Tables VIII, IX, and X under the
 same sequence name as mentioned above. Notice that
 5 the only area of HIV-1 BRU which is predicted by the
 Lupas algorithm to contain a coiled-coil region, is
 from amino acids 635-670. This begins eight amino
 acids N-terminal to the start and ends eight amino
 acids N-terminal to the end of DP178. DP107, despite
 10 the fact that it is a known coiled coil, is not
 predicted to contain a coiled-coil region using the
 Lupas method.

11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION
 15 OF DP107-LIKE AND DP178-LIKE
 SEQUENCES IN HUMAN RESPIRATORY
SYNCYTIAL VIRUS

FIG. 21 represents search results for Human
 Respiratory Syncytial Virus (RSV; Strain A2) fusion
 glycoprotein F1 (PC/Gene protein sequence name PVGLF_
 20 HRSVA). Motif 107x178x4 finds three hits including
 amino acids 152-202, 213-243, and 488-515. The
 arrangement of these hits is similar to what is found
 in HIV-1 except that the motif finds two regions with
 25 similarities to DP-178, one just downstream of what
 would be called the DP107 region or amino acids 213-
 243, and one just upstream of the transmembrane region
 (also similar to DP178) or amino acids 488-515. Motif
 ALLMOTI5 also finds three areas including amino acids
 30 116-202, 267-302, and 506-549. The proline-leucine
 zipper motifs also gave several hits including amino
 acids 205-221 and 265-287 (P1LZIPC 265-280, P12LZIPC),
 and 484-513 (P7LZIPC and P12LZIPC 484-506, P23LZIPC).
 Notice that the PLZIP motifs also identify regions
 35 which share location similarities with DP-178 of HIV-
 1.

12. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP107-LIKE AND DP178-LIKE SEQUENCES
IN SIMIAN IMMUNODEFICIENCY VIRUS

Motif hits for Simian immunodeficiency Virus gp41
(AGM3 isolate; PC/Gene protein sequence name
5 PENV_SIVAG) are shown in FIG. 22. Motif 107x178x4
finds three hits including amino acids 566-593, 597-
624, and 703-730. The first two hits only have three
amino acids between them and could probably be
combined into one hit from 566-624 which would
10 represent a DP107-like hit. Amino acids 703 to 730
would then represent a DP178-like hit. ALLMOTI5 also
finds three hits including amino acids 556-628 (DP107-
like), 651-699 (DP178-like), and 808-852 which
represents the transmembrane spanning region. SIV
15 also has one region from 655-692 with a high
propensity to form a coiled coil as predicted by the
Lupas algorithm. Both 107x178x4 and ALLMOTI5 motifs
find the same region. SIV does not have any PLZIP
motif hits in gp41.
20 The identification of DP178/DP107 analogs for a
second SIV isolate (MM251) is demonstrated in the
Example presented, below, in Section 19.

13. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP107-LIKE AND DP178 LIKE SEQUENCES
25 IN CANINE DISTEMPER VIRUS

Canine Distemper Virus (strain Onderstepoort)
fusion glycoprotein F1 (PC/Gene Protein sequence name
PVGLF_CDVO) has regions similar to Human RSV which are
30 predicted to be DP107-like and DP178-like (FIG. 23).
Motif 107x178x4 highlights one area just C-terminal to
the fusion peptide at amino acids 252-293. Amino
acids 252-286 are also predicted to be coiled coil
using the Lupas algorithm. Almost 100 amino acids C-
35 terminal to the first region is a DP178-like area at
residues 340-367. ALLMOTI5 highlights three areas of

interest including: amino acids 228-297, which completely overlaps both the Lupas prediction and the DP107-like 107x178x4 hit; residues 340-381, which overlaps the second 107x178x4 hit; and amino acids 568-602, which is DP178-like in that it is located just N-terminal to the transmembrane region. It also overlaps another region (residues 570-602) predicted by the Lupas method to have a high propensity to form a coiled coil. Several PLZIP motifs successfully identified areas of interest including P6 and P12LZIPC which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residues 398-414; and P12 and P23LZIPC which find residues 562-589 and 562-592 respectively.

14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN NEWCASTLE DISEASE VIRUS

FIG. 24 shows the motif hits found in Newcastle Disease Virus (strain Australia-Victoria/32; PC Gene protein sequence name PVGLF_NDVA). Motif 107x178x4 finds two areas including a DP107-like hit at amino acids 151-178 and a DP178-like hit at residues 426-512. ALLMOTIS finds three areas including residues 117-182, 231-272, and 426-512. The hits from 426-512 include a region which is predicted by the Lupas method to have a high coiled-coil propensity (460-503). The PLZIP motifs identify only one region of interest at amino acids 273-289 (P1 and 12LZIPC).

15. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES IN HUMAN PARAINFLUENZA VIRUS

Both motifs 107x178x4 and ALLMOTIS exhibit DP107-like hits in the same region, 115-182 and 117-182 respectively, of Human Parainfluenza Virus (strain NIH 47885; PC/Gene protein sequence name PVGLF_p13H4;

(FIG. 25). In addition, the two motifs have a DP178-like hit just slightly C-terminal at amino acids 207-241. Both motifs also have DP178-like hits near the transmembrane region including amino acids 457-497 and 462-512 respectively. Several PLZIP motif hits are also observed including 283-303 (P5LZIPC), 283-310 (P12LZIPC), 453-474 (P6LZIPC), and 453-481 (P23LZIPC). The Lupas algorithm predicts that amino acids 122-176 may have a propensity to form a coiled-coil.

10 16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP107-LIKE AND DP178-LIKE SEQUENCES OF INFLUENZA A VIRUS

FIG. 26 illustrates the Lupas prediction for a coiled coil in Influenza A Virus (strain A/Aichi/2/68) at residues 379-436, as well as the motif hits for 107x178x4 at amino acids 387-453, and for ALLMOTIS at residues 380-456. Residues 383-471 (38-125 of HA2) were shown by Carr and Kim to be an extended coiled coil when under acidic pH (Carr and Kim, 1993, Cell 73: 823-832). The Lupas algorithm predicts a coiled-coil at residues 379-436. All three methods successfully predicted the region shown to actually have coiled-coil structure; however, ALLMOTIS predicted the greatest portion of the 88 residue stretch.

17. EXAMPLE: POTENTIAL RESPIRATORY SYNCYTIAL VIRUS DP178/DP107 ANALOGS: CD AND ANTIVIRAL CHARACTERIZATION

In the Example presented herein, respiratory syncytial virus (RSV) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 11, above, were tested for anti-RSV activity. Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated

that several of the identified peptides exhibit potential antiviral capability. Additionally, it is shown that several of these peptides exhibit a substantial helical character.

5

17.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in Section 6.1. Peptide concentrations were determined from A_{210} using Edlehoch's method (1967, Biochemistry 6:1948).

10

Anti-RSV antiviral activity assays: The assay utilized herein tested the ability of the peptides to disrupt the ability of HEp2 cells acutely infected with RSV (i.e., cells which are infected with a multiplicity of infection of greater than 2) to fuse and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. The lower the observed level of fusion, the greater the antiviral activity of the peptide was determined to be.

15

Uninfected confluent monolayers of Hep-2 cells were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 3%, antibiotics (penicillin/streptomycin; Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

20

To prepare Hep2 cells for addition to uninfected cells, cultures of acutely infected Hep2 cells were

25

washed with DPBS (Dulbecco's Phosphate Buffered Saline w/ calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected Hep-2 cells.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Hep-2 cells, then adding peptides (at the dilutions described below) in 3% EMEM, and 100 acutely RSV-infected Hep2 cells per well. Wells were then incubated at 37°C for 48 hours.

After incubation, cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of either Crystal Violet stain or XTT. With respect to Crystal Violet, approximately 50µl 0.25% Crystal Violet stain in methanol were added to each well. The wells were rinsed immediately, to remove excess stain, and were allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

With respect to XTT (2,3-bis[2-Methoxy-4-nitro-5-sulfophenyl]-2H-tetrazolium-5-carboxyanilide inner salt), 50µl XTT (1mg/ml in RPMI buffered with 100mM HEPES, pH 7.2-7.4, plus 5% DMSO) were added to each well. The OD_{450/690} was measured (after blanking against growth medium without cells or reagents, and against reagents) according to standard procedures.

Peptides: The peptides characterized in the study presented herein were:

1) peptides T-142 to T-155 and T-575, as shown in FIG. 27A, and peptides T-22 to T-27, T-68, T-334 and T-371 to T-375 and T-575, as shown in FIG. 27B;

2) peptides T-120 to T-141 and T-576, as shown in FIG. 27B, and peptides T-12, T-13, T-15, T-19, T-28 to T-30, T-66, T-69, T-70 and T-576, as shown in FIG. 27D; and

3) peptides T-67 and T-104 to T-119 and T-384, as shown in FIG. 28A, and peptides T-71, T-613 to T-617, T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions of the RSV F2 protein DP178/107-like region. The peptides of group 2 represent portions of the RSV F1 protein DP107-like region. The peptides of groups 3 represent portions of the RSV F1 protein DP178-like region.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used. The IC₅₀ data for each peptide represents the average of several experiments conducted utilizing that peptide.

17.2 RESULTS

The data summarized in FIGS. 27A-B and 28A-B represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RSV F1 DP-107-like region (FIG. 27C-D) and the RSV DP178-like F2 region (FIG. 28A-B).

As shown in FIGS. 27A-D, a number of the RSV DP178/DP107-like peptides exhibited a detectable level of antiviral activity. Peptides from the RSV DP178/DP107-like F2 region (FIG. 27A-B), for example, T-142 to T-145 and T-334 purified peptides, exhibited detectable levels of antiviral activity, as evidenced by their IC₅₀ values. Further, a number of RSV F1 DP107-like peptides (FIG. 27C-D) exhibited a sizable level of antiviral activity as purified peptides, including, for example, peptides T-124 to T-127, T-

131, T-135 and T-137 to T-139, as demonstrated by their IC_{50} values. In addition, CD analysis FIG. 27A, 27C) reveals that many of the peptides exhibit some detectable level of helical structure.

5 The results summarized in FIG. 28A-B demonstrate that a number of DP178-like purified peptides exhibit a range of potent anti-viral activity. These peptides include, for example, T-67, T-104, T-105 and T-107 to T-119, as listed in FIG. 28A, and T-665 to T-669 and T-671 to T-673, as listed in FIG. 28B. In addition,
10 some of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, successfully identified viral peptide domains that represent highly promising anti-RSV
15 antiviral compounds.

18. EXAMPLE: POTENTIAL HUMAN PARAINFLUENZA VIRUS
TYPE 3 DP178/DP107 ANALOGS: CD AND
ANTIVIRAL CHARACTERIZATION

20 In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 15, above, were tested for anti-HPIV3 activity.
25 Additionally, circular dichroism (CD) structural analyses were conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that several of
30 these peptides exhibit a substantial helical character.

18.1 MATERIALS AND METHODS

Structural analyses: Structural analyses
35 consisted of circular dichroism (CD) studies. The CD

spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell in a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were
5 determined from A_{280} using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-HPiV3 antiviral activity assays: The assay utilized herein tested the ability of the peptides to
10 disrupt the ability of Hep2 cells chronically infected with HPiV3 to fuse and cause syncytial formation on a monolayer of an uninfected line of CV-1W cells. The more potent the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of CV-1W cells
15 were grown in microtiter wells in 3% EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum [FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented
20 at 3%, antibiotics/antimycotics (Gibco BRL Life Technologies Cat. No. 15040-017) added at 1%, and glutamine added at 1%.

To prepare Hep2 cells for addition to uninfected cells, cultures of chronically infected Hep2 cells
25 were washed with DPBS (Dulbecco's Phosphate Buffered Saline w/o calcium or magnesium; Bio Whittaker Cat. No. 17-512F) and cell monolayers were removed with Versene (1:5000; Gibco Life Technologies Cat. No. 15040-017). The cells were spun 10 minutes and
30 resuspended in 3% FBS. Cell counts were performed using a hemacytometer. Persistent cells were added to the uninfected CV-1W cells.

The antiviral assay was conducted by, first, removing all media from the wells containing
35 uninfected CV-1W cells, then adding peptides (at the

dilutions described below) in 3% EMEM, and 500 chronically HPIV3-infected Hep2 cells per well. Wells were then incubated at 37°C for 24 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50 µl 0.25% Crystal Violet stain in methanol. Wells were rinsed immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Alternatively, instead of Crystal Violet analysis, cells were assayed with XTT, as described, above, in Section 17.1.

Peptides: The peptides characterized in the study presented herein were:

- 1) Peptides 157 to 188, as shown in FIG. 29A, and peptides T-38 to T-40, T-42 to T-46 and T-582, as shown in FIG. 29B. These peptides are derived from the DP107 region of the HPIV3 F1 fusion protein (represented by HPF3 107, as shown in FIG. 29A); and
- 2) Peptides 189 to 210, as shown in FIG. 30A, and T-269, T-626, T-383 and T-577 to T-579, as shown in FIG. 30B. These peptides are primarily derived from the DP178 region of the HPIV3 F1 fusion protein (represented by HPF3 178, as shown in FIG. 30A). Peptide T-626 contains two mutated amino acid residues (represented by a shaded background). Additionally, peptide T-577 represents F1 amino acids 65-100, T-578 represents F1 amino acids 207-242 and T-579 represents F1 amino acids 273-309.

Each peptide was tested at 2-fold serial dilutions ranging from 500 µg/ml to approximately

500ng/ml. For each of the assays, a well containing no peptide was also used.

18.2 RESULTS

5 The data summarized in FIGS. 29A-B and 30A-B represent antiviral and structural information obtained from peptides derived from the HPIV3 fusion protein DP107-like region (FIG. 29A-B) and the HPIV3 fusion protein DP178-like region (FIG. 30A-B).

10 As shown in FIG. 29A-B, a number of the HPIV3 DP107-like peptides exhibited potent levels of antiviral activity. These peptides include, for example, peptides T-40, T-172 to T-175, T-178, T-184 and T-185.

15 The results summarized in FIG. 30A-B demonstrate that a number of the DP178-like peptides tested exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to 211, as evidenced by their low IC_{50} values. In fact, peptides 201 to 205 exhibit IC_{50} values in the nanogram/ml
20 range. In addition, many of the DP178-like peptides exhibited some level of helicity.

Thus, the computer assisted searches described, hereinabove, have successfully identified viral peptide domains that represent highly promising anti-
25 HPIV3 antiviral compounds.

19. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN IMMUNODEFICIENCY VIRUS

30 FIG. 31 represents search results for SIV isolate MM251 (PC/Gene® protein sequence PENV_SIVM2). Both 107x178x4 and ALLMOTI5 search motifs identified two regions with similarities to DP107 and/or DP178.

The peptide regions found by 107x178x4 were located at amino acid residues 156-215 and 277-289.
35 The peptide regions found by ALLMOTI5 were located at

amino acid residues 156-219 and 245-286. Both motifs, therefore, identify similar regions.

Interestingly, the first SIV peptide region (i.e., from amino acid residue 156 to approximately amino acid residue 219) correlates with a DP107 region, while the second region identified (i.e., from approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the DP178 region of HIV. In fact, an alignment of SIV isolate MM251 and HIV isolate BRU, followed by a selection of the best peptide matches for HIV DP107 and DP178, reveals that the best matches are found within the peptide regions identified by the 107x178x4 and ALLMOTI5 search motifs.

It should be noted that a potential coiled-coil region at amino acid residues 242-282 is predicted by the Lupas program. This is similar to the observation in HIV in which the coiled-coil is predicted by the Lupas program to be in the DP178 rather than in the DP107 region. It is possible, therefore, that SIV may be similar to HIV in that it may contain a coiled-coil structure in the DP107 region, despite such a structure being missed by the Lupas algorithm. Likewise, it may be that the region corresponding to a DP178 analog in SIV may exhibit an undefined structure, despite the Lupas program's prediction of a coiled-coil structure.

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20. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP178/DP107 ANALOGS IN EPSTEIN-BARR
VIRUS**

The results presented herein describe the identification of DP178/DP107 analogs within two different Epstein-Barr Virus proteins. Epstein-Barr
5 is a human herpes virus which is the causative agent of, for example, infectious mononucleosis (IM), and is also associated with nasopharyngeal carcinomas (NPC), Burkitt's lymphoma and other diseases. The virus
10 predominantly exists in the latent form and is activated by a variety of stimuli.

FIG. 32 depicts the search motif results for the Epstein-Barr Virus (Strain B95-8; PC/Gene® protein sequence PVGLB_EBV) glycoprotein gp110 precursor
15 (gp115). The 107x178x4 motif identified two regions of interest, namely the regions covered by amino acid residues 95-122 and 631-658. One PZIP region was identified at amino acid residue 732-752 which is most likely a cytoplasmic region of the protein. The Lupas
20 algorithm predicts a coiled-coil structure for amino acids 657-684. No ALLMOTI5 regions were identified.

FIG. 33 depicts the search motif results for the Zebra (or EB1) trans-activator protein (BZLF1) of the above-identified Epstein-Barr virus. This protein is
25 a transcription factor which represents the primary mediator of viral reactivation. It is a member of the b-ZIP family of transcription factors and shares significant homology with the basic DNA-binding and dimerization domains of the cellular oncogenes c-fos and C/EBP. The Zebra protein functions as a
30 homodimer.

Search results demonstrate that the Zebra protein exhibits a single region which is predicted to be either of DP107 or DP178 similarity, and is found
35 between the known DNA binding and dimerization regions of the protein. Specifically, this region is located.

at amino acid residues 193-220, as shown in FIG. 33. The Lupas program predicted no coiled-coil regions.

21. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN MEASLES VIRUS

5 FIG. 34 illustrates the motif search results for the fusion protein F1 of measles virus, strain Edmonston (PC Gene® protein sequence PVGLF_MEASE), successfully identifying DP178/DP107 analogs.

10 The 107x178x4 motif identifies a single region at amino acid residues 228-262. The ALLMOTI5 search motif identifies three regions, including amino acid residues 116-184, 228-269 and 452-500. Three regions containing proline residues followed by a leucine zipper-like sequence were found beginning at proline
15 residues 214, 286 and 451.

The Lupas program identified two regions it predicted had potential for coiled-coil structure, which include amino acid residues 141-172 and 444-483.

20 22. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN HEPATITIS B VIRUS

FIG. 35 depicts the results of a PZIP motif search conducted on the Hepatitis B virus subtype AYW. Two regions of interest within the major surface
25 antigen precursor S protein were identified. The first lies just C-terminal to the proposed fusion peptide of the major surface antigen (Hbs) which is found at amino acid residues 174-191. The second region is located at amino acid residues 233-267. The
30 Lupas program predicts no coiled-coil repeat regions.

In order to test the potential anti-HBV antiviral activity of these DP178/DP107 analog regions, peptides derived from area around the analog regions are synthesized, as shown in FIG. 52A-B. These peptides
35 represent one amino acid peptide "walks" through the

putative DP178/DP107 analog regions. The peptides are synthesized according to standard Fmoc chemistry on Rinkamide MBHA resins to provide for carboxy terminal blockade (Chang, C.D. and Meinhofer, J., 1978, Int. J. Pept. Protein Res. 11:246-249; Fields, G.B. and Noble, R.L., 1990, Int. J. Pept. Protein Res. 35:161-214). Following complete synthesis, the peptide amino-terminus is blocked through automated acetylation and the peptide is cleaved with trifluoroacetic acid (TFA) and the appropriate scavengers (King, D.S. et al., 1990, Int. J. Pept. Res. 36:255-266). After cleavage, the peptide is precipitated with ether and dried under vacuum for 24 hours.

The anti-HBV activity of the peptides is tested by utilizing standard assays to determine the test peptide concentration required to cause an acceptable (e.g., 90%) decrease in the amount of viral progeny formed by cells exposed to an HBV viral inoculum. Candidate antiviral peptides are further characterized in model systems such as wood chuck tissue culture and animal systems, prior to testing on humans.

23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF DP178/DP107 ANALOGS IN SIMIAN MASON-PFIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simian Mason-Pfizer monkey virus. The motifs reveal DP178/DP107 analogs within the enveloped (TM) protein GP20, as shown in FIG. 36.

The 107x178x4 motifs identifies a region at amino acid residues 422-470. The ALLMOTI5 finds a region at amino acid residues 408-474. The Lupas program predicted a coiled-coil structure amino acids 424-459.

35

24. **EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP178/DP107 ANALOGS IN BACTERIAL
PROTEINS**

5 The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to sequences present in proteins of a variety of bacterial species.

10 FIG. 37 depicts the search motif results for the *Pseudomonas aeruginosa* fimbrial protein (Pilin). Two regions were identified by motifs 107x178x4 and ALLMOTI5. The regions located at amino acid residues 30-67 and 80-144 were identified by the 107x178x4 motif. The regions at amino acid residues 30-68 and 80-125 were identified by the ALLMOTI5.

15 FIG. 38 depicts the search motif results for the *Pseudomonas gonorrhoeae* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 66-97 was identified by the 107x178x4 motif. The region located at amino acid residues 66-125 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

20 FIG. 39 depicts the search motif results for the *Hemophilus Influenza* fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

25 FIG. 40 depicts the search motif results for the *Staphylococcus aureus* toxic shock syndrome Hemophilus Influenza fimbrial protein (Pilin). A single region was identified by both the 107x178x4 and the ALLMOTI5 motifs. The region located at amino acid residues 102-129 was identified by the 107x178x4 motif. The

region located at amino acid residues 102-148 were identified by the ALLMOTI5 search motif. No coiled-coil regions were predicted by the Lupas program.

FIG. 41 summarizes the motif search results conducted on the Staphylococcus aureus enterotoxin Type E protein. These results demonstrate the successful identification of DP178/DP107 analogs corresponding to peptide sequences within this protein, as described below.

The ALLMOTI5 motif identified a region at amino acid residues 22-27. The 107x178x4 motif identified two regions, with the first at amino acid residues 26-69 and the second at 88-115. A P12LZIPC motif search identified two regions, at amino acid residues 163-181 and 230-250.

The Lupas program predicted a region with a high propensity for coiling at amino acid residues 25-54. This sequence is completely contained within the first region identified by both ALLMOTI5 and 107x178x4 motifs.

FIG. 42 depicts the search motif results conducted on a second Staphylococcus aureus toxin, enterotoxin A. Two regions were identified by the ALLMOTI5 motif, at amino acid residues 22-70 and amino acid residues 164-205. The 107x178x4 motif found two regions, the first at amino acid residues 26-69 and the second at amino acid residues 165-192. A P23LZIPC motif search revealed a region at amino acid residues 216-250. No coiled-coil regions were predicted by the Lupas program.

FIG. 43 shows the motif search results conducted on the E. coli heat labile enterotoxin A protein, demonstrating that identification of DP178/DP107 analogs corresponding to peptides located within this protein. Two regions were identified by the ALLMOTI5 motif, with the first residing at amino acid residues

55-115, and the second residing at amino acid residues 216-254. The 107x178x4 motif identified a single region at amino acid residues 78-105. No coiled-coil regions were predicted by the Lupas program.

5 25. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION OF
DP178/DP107 ANALOGS WITHIN VARIOUS
HUMAN PROTEINS

The results presented herein demonstrate the identification of DP178/DP107 analogs corresponding to peptide sequences present within several different human proteins.

FIG. 44 illustrates the search motif results conducted on the human c-fos oncoprotein. The ALLMOTI5 motif identified a single region at amino acid residues 155-193. The 107x178x4 motif identified one region at amino acid residues 162-193. The Lupas program predicted a region at amino acid residues 148-201 to have coiled-coil structure.

FIG. 45 illustrates the search motif results conducted on the human lupus KU autoantigen protein P70. The ALLMOTI5 motif identified a single region at amino acid residues 229-280. The 107x178x4 motif identified one region at amino acid residues 235-292. The Lupas program predicted a region at amino acid residues 232-267 to have coiled-coil structure.

FIG. 46 illustrates the search motif results conducted on the human zinc finger protein 10. The ALLMOTI5 motif identified a single region at amino acid residues 29-81. The 107x178x4 motif identified one region at amino acid residues 29-56. A P23LZIPC motif search found a single region at amino acid residues 420-457. The Lupas program predicted no coiled-coil regions.

26. EXAMPLE: POTENTIAL MEASLES VIRUS DP178/DP107
ANALOGS: CD AND ANTIVIRAL
CHARACTERIZATION

In the Example presented herein, measles (MeV) virus DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9 and 21, above, are tested for anti-MeV activity. Additionally, circular dichroism (CD) structural analyses are conducted on the peptides, as discussed below. It is demonstrated that several of the identified peptides exhibit potent antiviral capability. Additionally, it is shown that none of the these peptides exhibit a substantial helical character.

26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell on a Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from A_{280} using Edlehoch's method (1967, Biochemistry 6:1948).

Anti-MeV antiviral activity syncytial reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of Vero cells acutely infected with MeV (i.e., cells which are infected with a multiplicity of infection of 2-3) to fuse and cause syncytial formation on a monolayer of an uninfected line of Vero cells. The more potent the peptide, the lower the observed level of fusion, the greater the antiviral activity of the peptide.

Uninfected confluent monolayers of Vero cells were grown in microtiter wells in 10% FBS EMEM (Eagle Minimum Essential Medium w/o L-glutamine [Bio Whittaker Cat. No. 12-125F], with fetal bovine serum

[FBS; which had been heat inactivated for 30 minutes at 56°C; Bio Whittaker Cat. No. 14-501F) supplemented at 10%, antibiotics/antimycotics (Bio Whittaker Cat. No. 17-602E) added at 1%, and glutamine added at 1%.

To prepare acutely infected Vero cells for addition to the uninfected cells, cultures of acutely infected Vero cells were washed twice with HBSS (Bio Whittaker Cat. No. 10-543F) and cell monolayers were removed with trypsin (Bio Whittaker Cat. No. 17-161E). Once cells detached, media was added, any remaining clumps of cells were dispersed, and hemacytometer cell counts were performed.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and 50-100 acutely MeV-infected Vero cells per well. Wells were then incubated at 37°C for a maximum of 18 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50 µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Anti-MeV antiviral activity plaque reduction assay: The assay utilized herein tested the ability of the peptides to disrupt the ability of MeV to infect permissive, uninfected Vero cells, leading to the infected cells' fusing with uninfected cells to produce syncytia. The lower the observed level of syncytial formation, the greater the antiviral activity of the peptide.

Monolayers of uninfected Vero cells are grown as described above.

The antiviral assay was conducted by, first, removing all media from the wells containing uninfected Vero cells, then adding peptides (at the dilutions described below) in 10% FBS EMEM, and MeV stock virus at a final concentration of 30 plaque forming units (PFU) per well. Wells were then incubated at 37°C for a minimum of 36 hours and a maximum of 48 hours.

On day 2, after cells in control wells were checked for fusion centers, media was removed from the wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain in methanol. Wells were rinsed twice with water immediately, to remove excess stain and were then allowed to dry. The number of syncytia per well were then counted, using a dissecting microscope.

Peptides: The peptides characterized in the study presented herein were peptides T-252A0 to T-256A0, T-257B1/C1, and T-258B1 to T-265B0, and T-266A0 to T-268A0, as shown in FIG. 47. These peptides represent a walk through the DP178-like region of the MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

26.2 RESULTS

The data summarized in FIG. 47 represents antiviral and structural information obtained via "peptide walks" through the DP178-like region of the MeV fusion protein.

As shown in FIG. 47, the MeV DP178-like peptides exhibited a range of antiviral activity as crude peptides. Several of these peptides were chosen for purification and further antiviral characterization.

The IC₅₀ values for such peptides were determined, as shown in FIG. 47, and ranged from 1.35µg/ml (T-257B1/C1) to 0.072µg/ml (T-265B1). None of the DP178-like peptides showed, by CD analysis, a detectable level of helicity.

5 Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified viral peptide domains that represent highly promising anti-MeV antiviral compounds.

10

27. EXAMPLE: POTENTIAL SIV DP178/DP107 ANALOGS:
ANTIVIRAL CHARACTERIZATION

In the Example presented herein, simian immunodeficiency virus (SIV) DP178-like peptides identified by utilizing the computer-assisted search motifs described in the Examples presented in Sections 9, 12 and 19, above, were tested for anti-SIV activity. It is demonstrated that several of the identified peptides exhibit potent antiviral capability.

20

27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay utilized herein were as reported in Langolis et al. (Langolis, A.J. et al., 1991, AIDS Research and Human Retroviruses 7:713-720).

Peptides: The peptides characterized in the study presented herein were peptides T-391 to T-400, as shown in FIG. 48. These peptides represent a walk through the DP178-like region of the SIV TM protein.

30

Each peptide was tested at 2-fold serial dilutions ranging from 100µg/ml to approximately 100ng/ml. For each of the assays, a well containing no peptide was also used.

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27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide walks" through the DP178-like region of the SIV TM protein.

5 As shown in FIG. 48, peptides T-391 to T-400 were tested and exhibited a potent antiviral activity as crude peptides.

Thus, the computer assisted searches described, hereinabove, as in for example, the Example presented in Section 9, for example, successfully identified
10 viral peptide domains that represent highly promising anti-SIV antiviral compounds.

28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 AND DP-178 PEPTIDE TRUNCATIONS AND MUTATIONS

15 The Example presented in this Section represents a study of the antiviral activity of DP107 and DP178 truncations and mutations. It is demonstrated that several of these DP107 and DP178 modified peptides exhibit substantial antiviral activity.

20

28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays performed were as those described, above, in Section 6.1. Assays utilized HIV-1/IIIB and/or HIV-2 NIH2 isolates.
25 Purified peptides were used, unless otherwise noted in FIGS. 49A-C.

Peptides: The peptides characterized in the study presented herein were:

- 30 1) FIGS. 49A-C present peptides derived from the region around and containing the DP178 region of the HIV-1 BRU isolate. Specifically, this region spanned from gp41 amino acid residue 615 to amino acid residue 717. The peptides listed contain
35 truncations of this region and/or mutations

which vary from the DP178 sequence amino acid sequence. Further, certain of the peptides have had amino- and/or carboxy-terminal groups either added or removed, as indicated in the figures; and

- 5 2) FIG. 50. presents peptides which represent truncations of DP107 and/or the gp41 region surrounding the DP107 amino acid sequence of HIV-1 BRU isolate. Certain of the peptides are unblocked or biotinylated, as indicated
10 in the figure.

Blocked peptides contained an acyl N-terminus and an amido C-terminus.

28.2 RESULTS

15 Anti-HIV antiviral data was obtained with the group 1 DP178-derived peptides listed in FIG. 49A-C. The full-length, non-mutant DP178 peptide (referred to in FIG. 49A-C as T20) results shown are for 4ng/ml.

20 In FIG. 49A, a number of the DP178 truncations exhibited a high level of antiviral activity, as evidenced by their low IC_{50} values. These include, for example, test peptides T-50, T-624, T-636 to T-641, T-645 to T-650, T-652 to T-654 and T-656. T-50
25 represents a test peptide which contains a point mutation, as indicated by the residue's shaded background. The HIV-1-derived test peptides exhibited a distinct strain-specific antiviral activity, in that none of the peptides tested on the HIV-2 NIH2 isolate demonstrated appreciable anti-HIV-2 antiviral
30 activity.

35 Among the peptides listed in FIG. 49B, are test peptides representing the amino (T-4) and carboxy (T-3) terminal halves of DP178 were tested. The amino terminal peptide was not active ($IC_{50} > 400 \mu\text{g/ml}$) whereas the carboxy terminal peptide showed potent antiviral

activity (IC_{50} = 3 μ g/ml). A number of additional test peptides also exhibited a high level of antiviral activity. These included, for example, T-61/T-102, T-217 to T-221, T-235, T-381, T-677, T-377, T-590, T-378, T-591, T-271 to T-272, T-611, T-222 to T-223 and
5 T-60/T-224. Certain of the antiviral peptides contain point mutations and/or amino acid residue additions which vary from the DP178 amino acid sequence.

In FIG. 49C, point mutations and/or amino and/or carboxy-terminal modifications are introduced into the
10 DP178 amino acid sequence itself. As shown in the figure, the majority of the test peptides listed exhibit potent antiviral activity.

Truncations of the DP107 peptide (referred to in FIG. 50 as T21) were also produced and tested, as shown
15 in FIG. 50. FIG. 50 also presents data concerning blocked and unblocked peptides which contain additional amino acid residues from the gp41 region in which the DP107 sequence resides. Most of these peptides showed antiviral activity, as evidenced by
20 their low IC_{50} values.

Thus, the results presented in this Section demonstrate that not only do the full length DP107 and DP178 peptides exhibit potent antiviral activity, but
25 truncations and/or mutant versions of these peptides can also possess substantial antiviral character.

29: EXAMPLE: POTENTIAL EPSTEIN-BARR DP178/DP107
ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, peptides derived
30 from the Epstein-Barr (EBV) DP-178/DP107 analog region of the Zebra protein identified, above, in the Example presented in Section 20 are described and tested for anti-EBV activity. It is demonstrated that among these peptides are ones which exhibit potential anti-
35 viral activity.

29.1 MATERIALS AND METHODS

Electrophoretic Mobility Shift Assays (EMSA):

Briefly, an EBV Zebra protein was synth sized utilizing SP6 RNA polymerase in vitro transcription and wheat germ in vitro translation systems (Promega Corporation recommendations; Butler, E.T. and Chamberlain, M.J., 1984, J. Biol. Chem. 257:5772; Pelham, H.R.B. and Jackson, R.J., 1976, Eur. J. Biochem. 67:247). The in vitro translated Zebra protein was then preincubated with increasing amounts of peptide up to 250 ng/ml prior to the addition of 10,000 to 20,000 c.p.m. of a ³²P-labeled Zebra response element DNA fragment. After a 20 minute incubation in the presence of the response element, the reaction was analyzed on a 4% non-denaturing polyacrylamide gel, followed by autoradiography, utilizing standard gel-shift procedures. The ability of a test peptide to prevent Zebra homodimer DNA binding was assayed by the peptide's ability to abolish the response element gel migration retardation characteristic of a protein-bound nucleic acid molecule.

Peptides: The peptides characterized in this study represent peptide walks through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. Specifically, the peptide walks covered the region from amino acid residue 173 to amino acid residue 246 of the EBV Zebra protein.

Each of the tested peptides were analyzed at a range of concentrations, with 150ng/ml being the lowest concentration at which any of the peptides exerted an inhibitory effect.

29.2 RESULTS

Th EBV Zebra protein transcription factor contains a DP178/DP107 analog region, as demonstrated in the Example presented, above, in Section 20. This protein appears to be the primary factor responsible for the reactivation capability of the virus. A method by which the DNA-binding function of the Zebra virus may be abolished may, therefore, represent an effective antiviral technique. In order to identify potential anti-EBV DP178/DP107 peptides, therefore, peptides derived from the region identified in Section 20, above, were tested for their ability to inhibit Zebra protein DNA binding.

The test peptides' ability to inhibit Zebra protein DNA binding was assayed via the EMSA assays described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results of EMSA assays of the listed EBV test peptides. These peptides represent one amino acid "walks" through the region containing, and flanked on both sides by, the DP178/DP107 analog region identified in the Example presented in Section 20, above, and shown as shown in FIG. 33. As shown in FIG. 51A-B, the region from which these peptides are derived lies from EBV Zebra protein amino acid residue 173 to 246. A number of the test peptides which were assayed exhibited an ability to inhibit Zebra protein homodimer DNA binding, including 439, 441, 444 and 445.

Those peptides which exhibit an ability to inhibit Zebra protein DNA binding represent potential anti-EBV antiviral compounds whose ability to inhibit EBV infection can be further characterized.

The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects

f th inv ntion, and functionally equivalent methods
and comp nents are within the sc pe of the invention.
Indeed, various modificati ns f the invention, in
addition to those shown and described herein will
become apparent to those skilled in the art from the
5 foregoing description and accompanying drawings. Such
modifications are intended to fall within the scope of
the appended claims.

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WHAT IS CLAIMED IS:

1. An isolated peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif.
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2. The peptide of Claim 1 wherein the peptide corresponds to a peptide present in a virus.
3. The peptide of Claim 2 in which the virus is
10 HIV-1 or HIV-2.
4. The peptide of Claim 2 in which the virus is a respiratory syncytial virus.
- 15 5. The peptide of Claim 2 in which the virus is a human parainfluenza virus.
6. The peptide of Claim 2 in which the virus is an influenza virus.
20
7. The peptide of Claim 2 in which the virus is a hepatitis B virus.
8. The peptide of Claim 2 wherein the virus is
25 an Epstein-Barr virus.
9. A method for the inhibition of transmission of a virus to a cell, comprising contacting the cell with an effective concentration of a peptide
30 recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search motif for an effective period of time so that no infection of the cell by the virus occurs.
10. The method of Claim 9 wherein the virus is
35 HIV-1 or HIV-2.

11. The method of Claim 9 wherein the virus is a respiratory syncytial virus.

12. The method of Claim 9 wherein the virus is a human parainfluenza virus.

5

13. The method of Claim 9 wherein the virus is an influenza virus.

14. The method of Claim 9 in which the virus is a hepatitis B virus.

10

15. The method of Claim 9 wherein the virus is an Epstein-Barr virus.

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HIV1LAI (DP-178; SEQ ID:1)	YTSLIHSLIEESQSQEKNQEQLLELDKWASLWNMF
HIV1SF2 (DP-185; SEQ ID:3)	YTNTIYNLLEESQSQEKNQEQLLELDKWASLWNMF
HIV1RF (SEQ ID:4)	YTGIIYNLLEESQSQEKNQEQLLELDKWANLWNMF
HIV1MN (SEQ ID:5)	YTSLIYSLLEKSQTQEQEKNQEQLLELDKWASLWNMF
HIV2ROD (SEQ ID:6)	LEANISKSLEQAQIQQEKINMYELOKLNWDIFGNMF
HIV2NIHZ (SEQ ID:7)	LEANISQSLEQAQIQQEKINMYELOKLNWDVFTNWIL
DP180 (SEQ ID:2)	SSSFITLLEQNNHKLQLAEQMLEQINEKHYLEDIS
DP118 (SEQ ID:10)	QQLLDWVKRQEQEMLRLTVWGTKNLQARVTAIEKYLKDQ
DP125 (SEQ ID:8)	CGGNLLRAIEAQQHLLQLTVWGIKQLQARILAVERYLKDQ
DP116 (SEQ ID:9)	LQARILAVERYLKDQQQ

FIG.1

7872-020 (SHEET 2 OF 63)

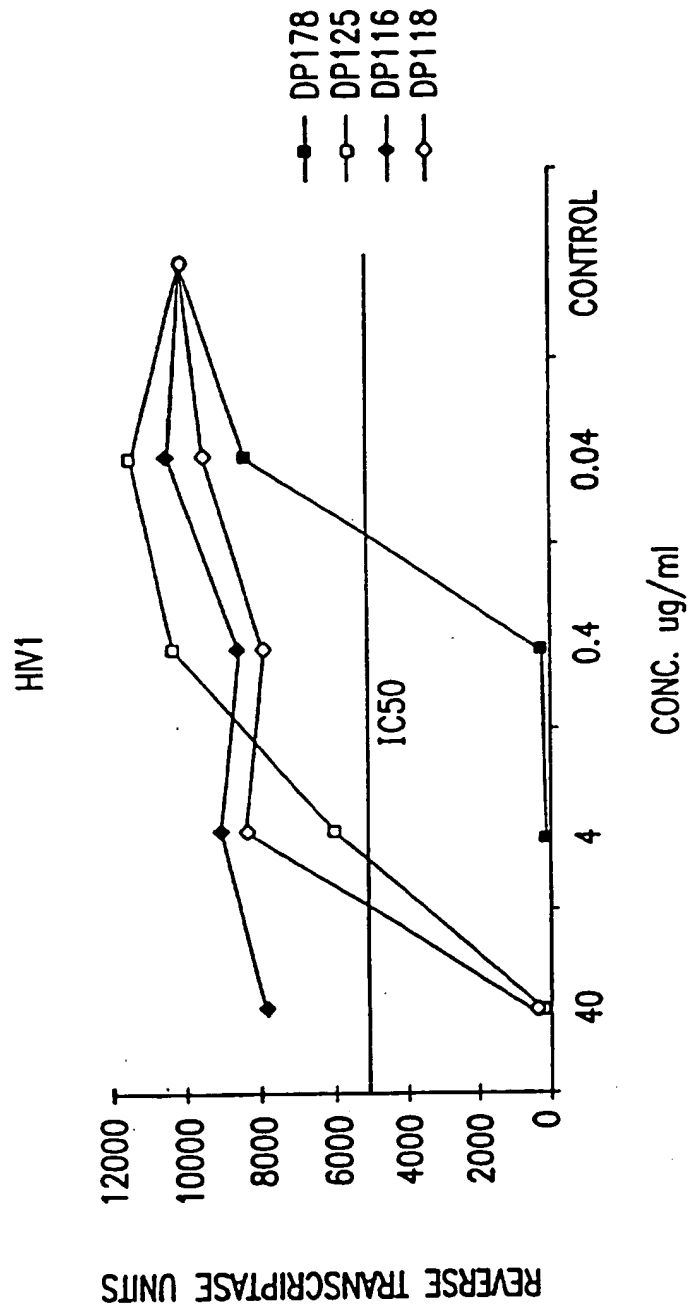


FIG.2

7872-020 (SHEET 3 OF 63)

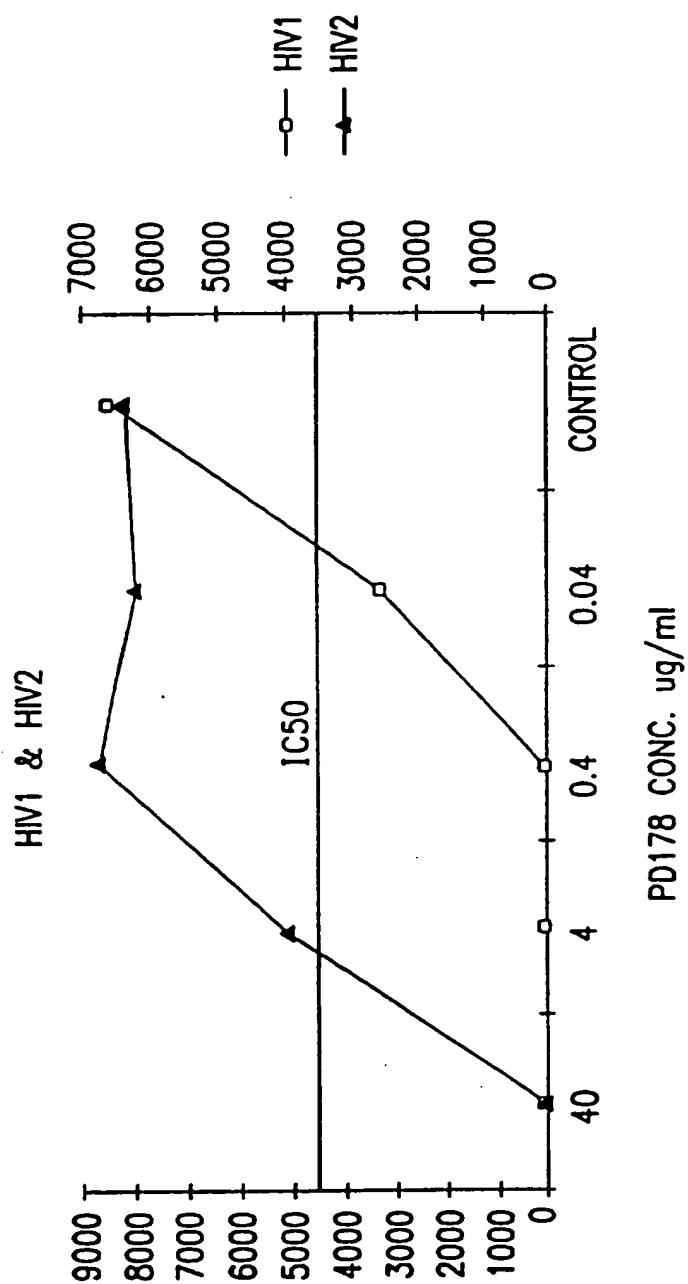


FIG.3

7872-020 (SHEET 4 OF 63)

Number of Syncytia/well: concentration in $\mu\text{g/ml}$ (micrograms/ml)									
DP178	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LA1	0	0	0	0	0	0	0	0	67
HIV1MN	0	0	0	0	0	ND	ND	ND	34
HIV1RF	0	0	0	0	0	ND	ND	ND	65
HIV1SF2	0	0	0	0	0	ND	ND	ND	58
DP125	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LA1	0	0	54	69	80	75	79	82	67
HIV1MN	0	0	30	36	ND	ND	ND	ND	34
HIV1RF	0	0	67	63	ND	ND	ND	ND	65
HIV1SF2	0	0	9	66	ND	ND	ND	ND	58
DP116	10	5	1	0.2	0.1	0.05	0.025	0.0125	Control
<i>Syncytia</i>									
HIV1LA1	75	ND	ND	ND	ND	ND	ND	ND	67
HIV1MN	35	ND	ND	ND	ND	ND	ND	ND	34
HIV1RF	81	ND	ND	ND	ND	ND	ND	ND	65
HIV1SF2	81	ND	ND	ND	ND	ND	ND	ND	58

FIG.4A

DP180	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncytia</i>									
HIV1LA1	50	>45	>45	>45	>45	>45	>45	>45	58
DP185	40	20	10	5	2.5	1.25	0.625	0.3125	Control
<i>Syncytia</i>									
HIV1LA1	0	0	0	0	0	0	0	ND	60

FIG.4B

7872-020 (SHEET 5 OF 63)

<u>HIV1</u>								
Number of Syncytio/well: concentration in ng/ml (nanograms/ml)								
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytio</u> <u>HIV1</u>	0	0	0	0	0	14	20	48
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytio</u> <u>HIV1</u>	ND	48	ND	ND	ND	ND	ND	ND
<u>HIV2</u>								
Number of Syncytio/well: concentration in μ g/ml (micrograms/ml)								
DP178	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytio</u> <u>HIV2</u>	50	54	55	57	63	77	78	76
DP116	20	10	5	2.5	1.25	0.625	0.3125	Control
<u>Syncytio</u> <u>HIV2</u>	ND	58	ND	ND	ND	ND	ND	ND

FIG.5

7872-020 (SHEET 6 OF 63)

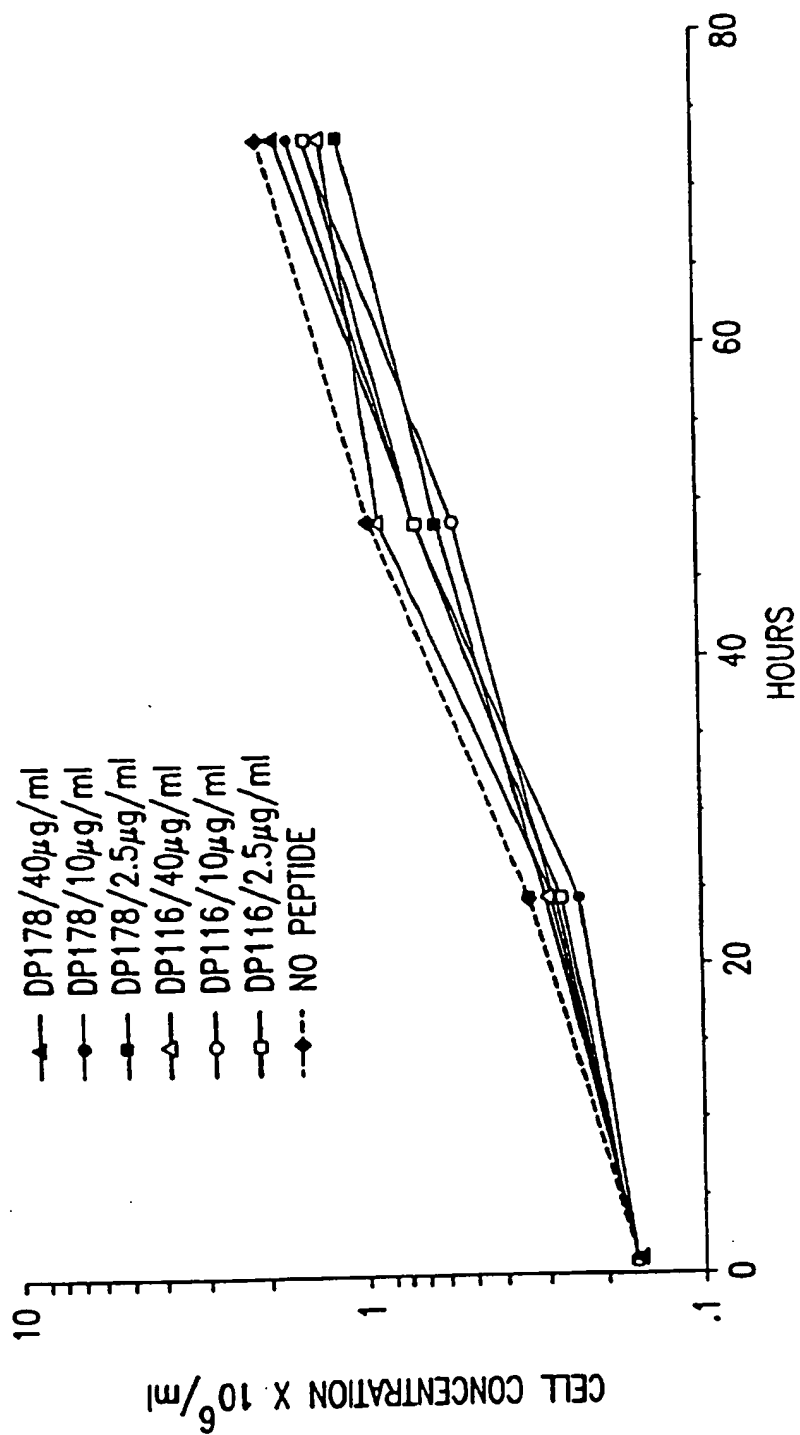


FIG.6

7872-020 (SHEET 7 OF 63)

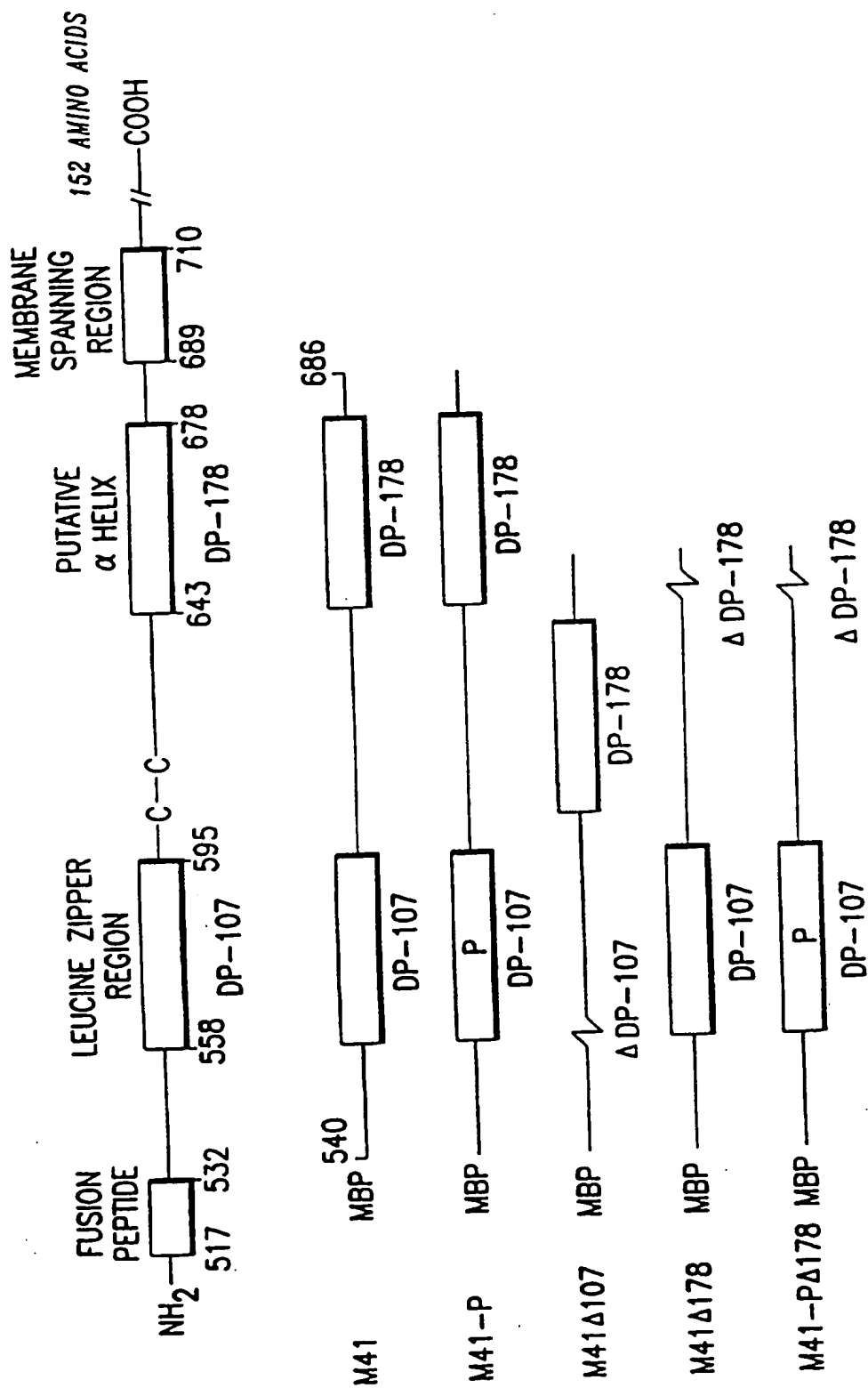


FIG. 7

7872-020 (SHEET 8 OF 63)

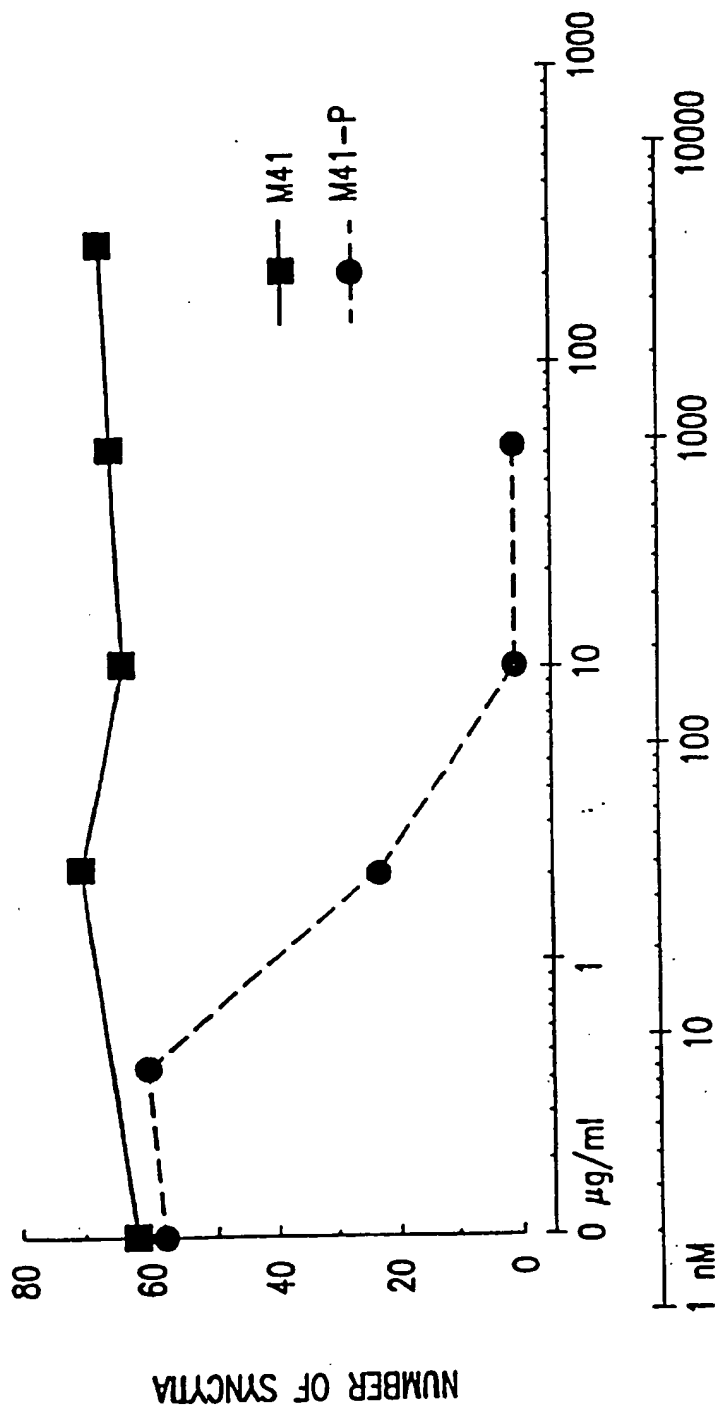


FIG.8

7872-020 (SHEET 9 OF 63)

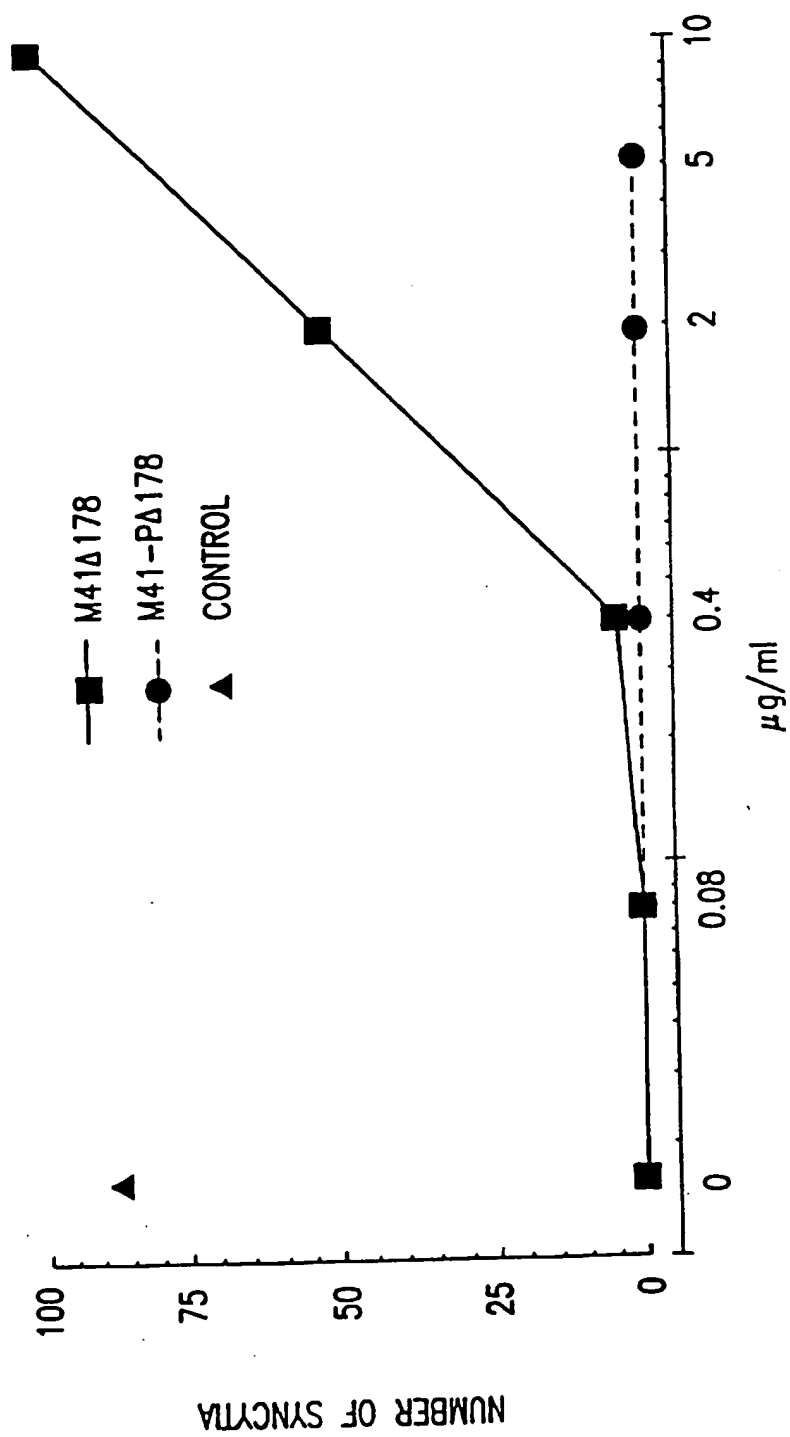


FIG.9

7872-020 (SHEET 10 OF 63)

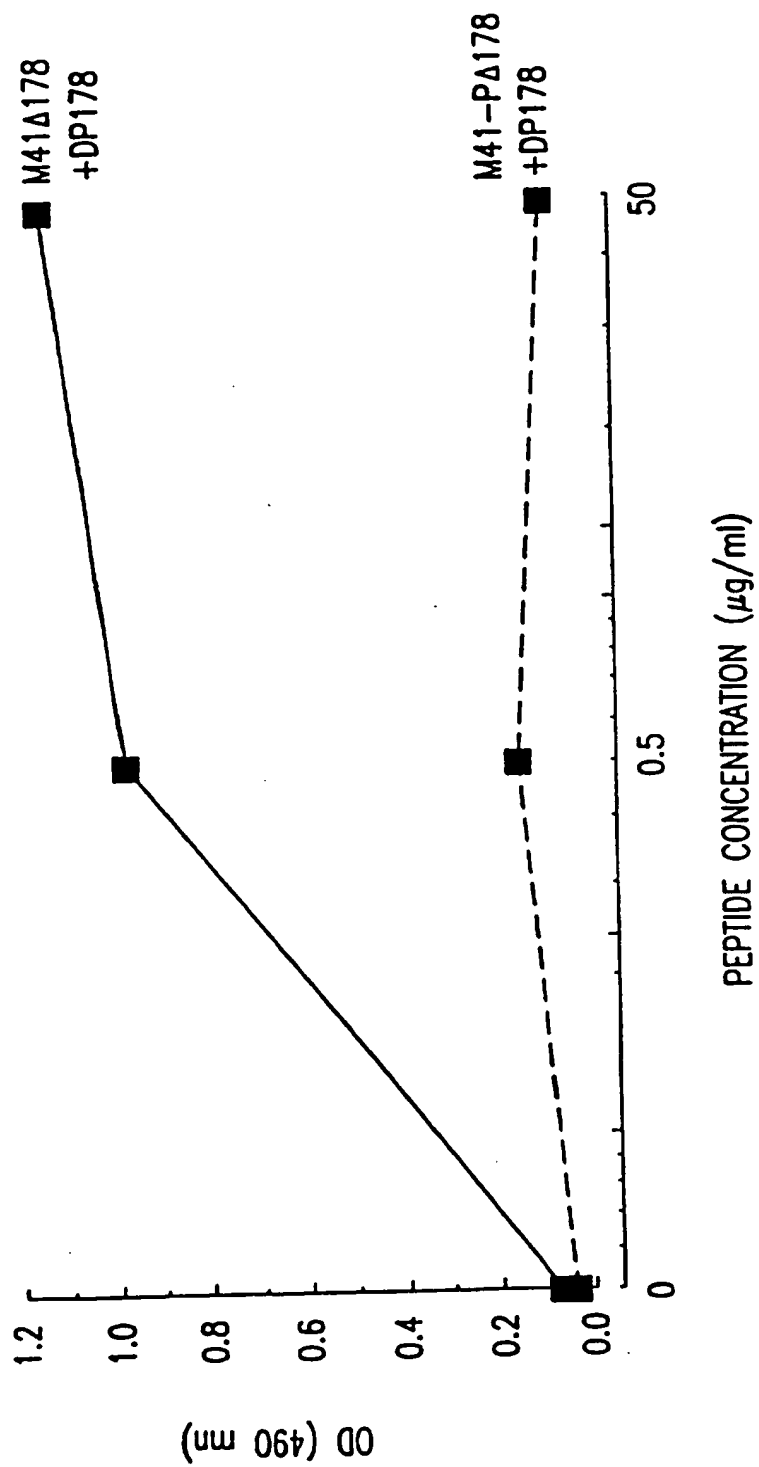


FIG.10

7872-020 (SHEET II OF 63)

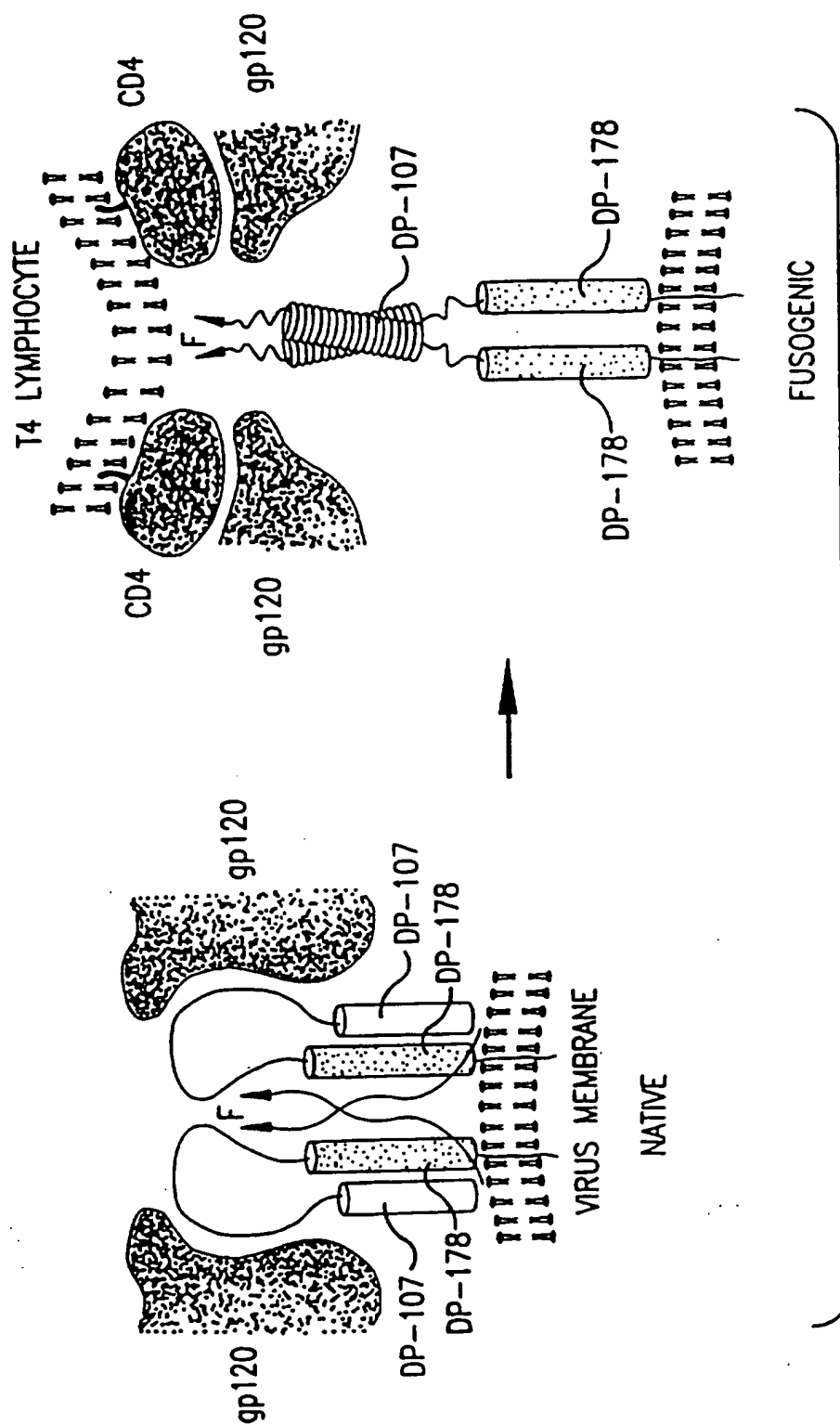
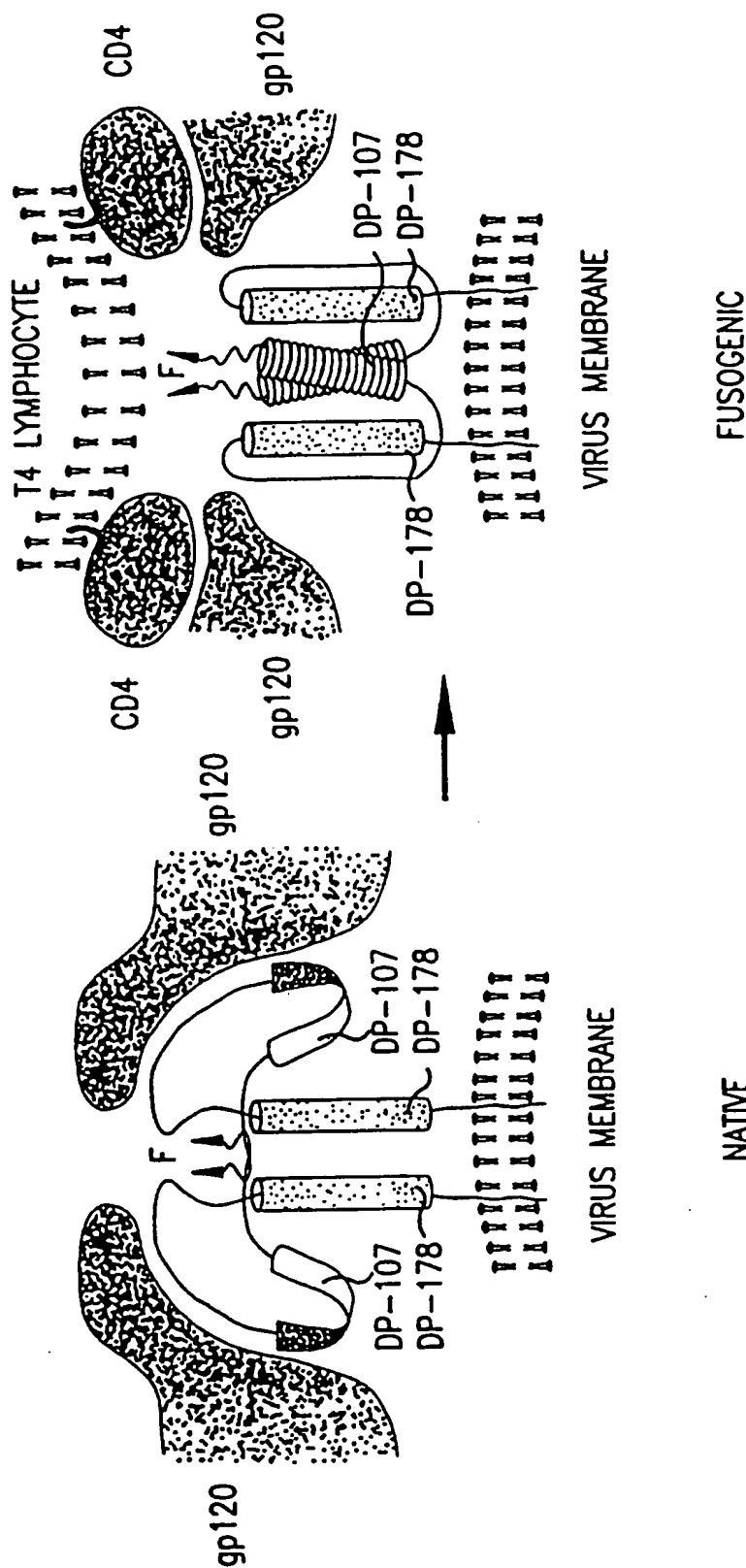


FIG.11A

7872-020 (SHEET 12 OF 63)



7872-020 (SHEET 17 OF 63)

Sequence	Positions																								Parent Motif	Hybrid Motif									
	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D					
DP-107 (env_hv1bru) L1=D	N	N	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	W	G	I	K	Q	L	A	V	E	R	Y	L	K	D	Q		[ILOIV] [CDFIMPST]		
DP-107 (env_hv1bru) L2=D	N	N	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	W	G	I	K	Q	L	A	V	E	R	Y	L	K	D	Q		[EKLNOV] [CFKAPS]		
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	Q	N	Q	E	K	N	E	Q	E	L	L	E	L	D	K	W	A	S	L	W	N	W	F	[EFKLOHY] [CFGAPRVY]
DP-178 (env_hv1bru) Y1=D																																	[EFILNDSWY] [CFGAPRVY]		
FLU LOOP 36	I	E	K	T	N	E	K	F	H	Q	I	E	K	E	F	S	E	V	E	G	R	I	Q	D	L	E	K	Y						[FILTV] [ACFLMPTVWH]	

Parent Motif

[ILQIV] {CDFIAPST}

[EKLNV] {CFKAPS}

[EFKLVY] {CFGPRVY}

[EFLNDSWY] {CFGPRVY}

[FILTV] {ACFLPTVH}

Hybrid Motif

[EFIKLNOSTVWY] {CFMP}

FIG.16

7872-020 (SHEET 18 OF 63)

Sequence	Positions												Parent Motif	Hybrid Motif																						
GCN4 (gcn4 yeast)	A	D	A	D	A	D	A	D	A	D	A	D	[LMNV] {CFGIMPVW}																							
DP-107 (env_hv1bru) L1=D	M	K	Q	L	E	D	K	V	E	E	L	L	S	K	N	Y	H	L	E	N	E	V	A	R	L	K	K	L								
DP-178 (env_hv1bru) Y1=A	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	W	G	I	K	Q	L	A	R	I	L	A	V	E	R	Y	L	K	D	D
	Y	T	S	L	I	M	S	L	I	E	S	N	Q	E	K	N	E	Q	E	L	L	E	L	D	K	W	A	S	L	W	N	W	F		[EFIKLMDTVWY] {CFMP}	
GCN4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	L	S	K	N	Y	H	L	E	N	E	V	A	R	L	K	K	L								
DP-107 (env_hv1bru) L1=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	W	G	I	K	Q	L	A	R	I	L	A	V	E	R	Y	L	K	D	D
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	N	Q	E	K	N	E	Q	E	L	L	E	L	D	K	W	A	S	L	W	N	W	F		[EFILMDSTVWY] {CFMP}	
GCN4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	L	S	K	N	Y	H	L	E	N	E	V	A	R	L	K	K	L								
DP-107 (env_hv1bru) L2=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	W	G	I	K	Q	L	A	R	I	L	A	V	E	R	Y	L	K	D	D
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	N	Q	E	K	N	E	Q	E	L	L	E	L	D	K	W	A	S	L	W	N	W	F		[EFKLMNDVWY] {CFMP}	
GCN4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	L	S	K	N	Y	H	L	E	N	E	V	A	R	L	K	K	L								
DP-107 (env_hv1bru) L2=D	N	N	L	L	R	A	I	E	A	Q	H	L	L	Q	L	T	V	W	G	I	K	Q	L	A	R	I	L	A	V	E	R	Y	L	K	D	D
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	N	Q	E	K	N	E	Q	E	L	L	E	L	D	K	W	A	S	L	W	N	W	F		[EFILMDSTVWY] {CFMP}	

FIG.17

7872-020 (SHEET 19 OF 63)

Sequence	Positions																Parent Motif	Hybrid Motif
	A	D	A	D	A	D	A	D	A	D	A	D	A	D	A	D		
GCN4 (gcn4 yeast)	M	K	Q	L	E	D	K	V	E	E	L	S	K	N	Y	H	L	[LMAV] {CFGIMPW}
DP-107 (env_hv1bru) L1=D	N	N	L	L	R	A	T	E	A	Q	H	L	L	Q	L	T	V	[ILOTV] {CDFIMPST}
DP-107 (env_hv1bru) L2=D	N	N	L	L	R	A	T	E	A	Q	H	L	L	Q	L	T	V	[EKLNOV] {CFKAPS}
DP-178 (env_hv1bru) Y1=A	Y	T	S	L	I	H	S	L	I	E	S	O	N	Q	E	K	N	[EFKLOHY] {CFGMPRVY}
DP-178 (env_hv1bru) Y1=D	Y	T	S	L	I	H	S	L	I	E	S	O	N	Q	E	K	N	[EFILNDSWY] {CFGMPRVY}
C-FOS (fos_human)	T	D	T	L	O	A	E	T	D	Q	L	E	D	E	K	S	A	[IKLT] {CFGHIMPRWY}
C-JUN (jun1_human)	I	A	R	L	E	E	K	V	K	T	L	K	A	Q	N	S	E	[AILNW] {CDFGHILPWY}
C-MYC (myo_human)	E	Q	K	L	I	S	E	E	D	L	L	E	K	R	R	E	Q	[ELR] {ACFGMPWY}
FLU LOOP 36	I	E	K	T	I	N	E	K	F	H	Q	I	E	K	E	F	S	[FILTV] {ACFLMPTWY}

[AEF IKLMNORSTWY] [CFP]
 = [CDGHP] [CFP]

FIG.18

7872-020 (SHEET 20 OF 63)

P-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-{P}(1)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-{P}(2)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-{P}(3)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-{P}(4)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-{P}(5)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-{P}(6)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-{P}(7)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-{P}(8)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-{P}(9)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-{P}(10)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-X(1,12)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]
 P-X(13,23)-[LIV]-{P}(6)-[LIV]-{P}(6)-[LIV]

FIG.19

7872-020 (SHEET 22 OF 63)

Fusion ♡ALLMOTIS♡
 Peptide ♡107x178x4♡
 ♡.....ELGEL LGVGSALAS GVA ♡YSKVLHLEGEVNIKSA

 ♡P1&12LZIPC♡
LLSTNKAVVS LSNGVSVLTS KVLDLKNIYD KQ ♡ ♡ LL ♡PIVNKQ

 ♡107x178x4♡
 SC ♡SISNIETVI ♡ EEQOKNNRLLLETTREESYNAG ♡ VITPVSTMLTNSELLSL

 ♡P1&12LZIPC♡
 ♡ALLMOTIS♡
 INDM ♡PI ♡TNDQKKLMSNNVQI V ♡ RQSYSI ♡ MS IKKEEVLAYV

VQ ♡ LPLYGVID TPCWKLHTSP LCTTNTKEGS NICLTRTDRG WYCDNAGSVS

FFPQAETCKV QSNRVFCDTM NSLTLPSEIN LCNVDIFNPK

YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG

IIKTFSNGCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

 ♡P7, 12, & 23LZIPC♡
 ♡107x178x4♡ ♡ALLMOTIS♡
 EPIINFYDPLVF ♡PSDE ♡EDASISOVNEKINOSLAE ♡I ♡ RKSDELL ♡

 ♡Transmembrane Region ♡
HNVNA ♡ GK STTN ♡ IMITLIVIVILLS LIAVGLLLY ♡ C ♡

KARSTPVTLS KDQLSGINNI AFSN

FIG. 21

7872-020 (SHEET 23 OF 63)

Fusion
 Peptide ♡ALLMOTIS♡ ♡107x178x4♡
FLGELG ♡AAGTAMGAAA ♡TALTVQSOHLLAGILOQOKNLLAAY

 ♡107x178x4♡
EAQ ♡ QQM ♡ LKLTIWGYKNLNARVTALEKYLEDOARLN ♡ AWG♡ CA

 ♡LVS Coiled-Coil♡
 ♡ALLMOTIS♡ ♡107x178x4♡
 WKQVCHTTVP WQWNNRTPDW ♡NNMT ♡WLE ♡WEROISYLEGNTT

 ♡107x178x4♡
TOLEEARAQEEKNLD ♡ AYOKLSS ♡ WSDFWSW♡ FDF ♡SKWLN ♡ILK

♡Transmembrane Region♡
IGELDVLGIGLRLLYTY ♡ XS ♡ CIARVRQGYSPSPQIHHP WKGPDPNAEG

PGEKGDKRKN SSEPWQKESG TAEWKS NWCK RL TNWCSISS IWL YNS

♡ALLMOTIS♡
 ♡CLTL LVHLRSAFY IQYGLGELKA AAQEAVVALA RLAQNAGYQIWL♡

ACRSAYRA IINSPRRVRQ GLEGILN

FIG. 22

7872-020 (SHEET 24 OF 63)

Fusion ♣ 107x178x4 ♣
 Peptide ♣ ALLMOTI5 ♣ *LVS Coiled-Coil*
EAG ♣ VYL AGVALGVATA AQITAGIALHQ ♣ *SNLNAQAIO

SLRTSLEQSNKAIEEIREATOETVIA * VOGVODY ♣ VNNEI ♣ VP

♣ ALLMOTI5 ♣
 ♣ 107x178x4 ♣
 ♣ P6 & 12LZIPC ♣

AMQHMSCELVGQRLGLRLLRYYTELLSIFGPSLRD ♣ PISA ♣ ♣ EISIQALYAL

GGEIHKILEKLGYSQSD ♣ MIALESRGIKTKI ♣ THVDLPGKF ILSISY

♣ P1 & 12LZIPC ♣
 ♣ PTLSEVKGVIVHRLEAV ♣ SYNIGSQEWYTTVPRYIATNGYLISNFDDESSCVFVS

ESAICQNSL YPMSPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA

NCASILCKCY STSTIINQSP DKLLTFIASD TCPLVEIDGA TIQVGGRQYT

LVS Coiled-Coil
 ♣ ALLMOTI5 ♣
 ♣ P12 & 23LZIPC ♣

DMVYEGKVAL G ♣ PAISLD ♣ RL * DVGTNLGNALKKLD DAKVLI ♣

♦ Transmembrane Region ♦

DSS ♣ NOILETYR RS ♣ * SFN ♦ EGSLLSVPILSCTAL ALLLLIYCC ♦

K RRYQQTLKQH TKVDPAFKPD LTGTSKSYVR SL

FIG. 23

7872-020 (SHEET 25 OF 63)

Fusion ♡ALLMOTIS♡
 Peptide ♡107x178x4♡
 ♡.....FIGAI IGSVALGVA TAAQITAASA LIQANQNAAN ♡ILRLKESITA

TIEAVHEVTDGLSOLAVA ♡ VG KM ♡ QQFVNDQFNNTAQELDCIKITQQV

 ♡ALLMOTIS♡
 GVELNLYLTELT TV FGPQITSPAL ♡TQLTIQALYNAGGNMDYLLTKLGVG

 ♡P1 & 12LZIPC♡
 NNQLSSLIGSGLIT GN ♡ ♡PILYDSQT QLLGIQVTLP SVGNLNNMRATYLET

 LSVST TKGFASALVP KVVVTQVGSVI EELDTSYCIE TDL DLYCTRI VTFPMSPGIY

 SCLNGNTSAC MYSKTEGALT TPYMTLKGSV IANCKMTTCR CADPPGHSQ

 ♡ALLMOTIS♡
 ♡107x178x4♡
 NYGEAVSLID RHSCN ♡ ♡VLSLD GITLRLSGEF DATYQKNISI LDSQVIVTG

 ♡LVS Coiled-Coil♡ ♡Trans-
 ♡NLDISTELGNV NNSISNALDK LEESNSKLDK VNVKLTSTSA ♡LIT ♡YLA

membrane Region ♡
LTATSLVCGITSLV ♡ ♡LACYLMY ♡ KQKAQQKTLLWLGNNTLGQMRATTKM

FIG. 24

7872-020 (SHEET 26 OF 63)

Fusion ♡ALLMOTIS♡
 Peptide ♡107x178x4♡ *LVS Coiled-Coil*
EEGGV ♡IG ♡TIALG *VATSAQITA AVALVEAKOARSDIEKLKE

AIRDTNKAVQSVQSSIGNLIVAIKSVQ* DYVNKE♡ ♡ IVPSIARLGCEAAG

♡ALLMOTIS♡
 ♡107x178x4♡
 LQLGIALTQH ♡♡YSELTNIEGDNIGSLOEKGIKLOGIASLYRTNITE♡ ♡

♡P5 & 12LZIPC♡
 IFTTSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL ♡PLLTRLNTQIYR

VDSISYNI+ QNREWYI+ PLPSHIMTKGAFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISQCPRTVVKSDIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKIITHKECNTIGINGMLFNTNKEGTLAFYTP

♡ALLMOTIS♡
 ♡107x178x4♡
 ♡P6 & 23LZIPC♡
 NDITLNNNSVALD ♡PIDI ♡SIELN ♡KAKSDLEESKEWI+ RRSNOKL÷

♡Transmembrane Region♡
DSIGNWHQSSTT ♡IIIY ♡ LIM IIILEIINVT II ♡ ILAVKYY ♡ R

IQKRNRVDQN DKPYVLTNK

FIG. 25

7872-020 (SHEET 27 OF 63)

Fusion
Peptide
.....GLEGAI AGFIENGWEGMIDGWYGFRRHQNSEGTG

♣107x178x4♣
♥ALLMOTIS♥
LVS Coiled-Coil
*Q ♥AADLKST ♣QAAIDQINGKLNRVIEKTEKTEHQIEKETSEVEGRIO

DLEKYYEDTKIDL* WSYNAELLVALENOHTI♣ DLT♥ DSEMKNLFETR

RQLRENAEEMGNGCFKIYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG

VELKSGYKDWILWISFAISCFLLCVVLLGFIMWACQRGNIRCNICI

FIG. 26

7872-020 (SHEET 28 OF 63)

RSV F2	AV	Purified SCAR (x 10 ³)	CD
T-143	++	39	++
T-143	++	31	++
T-144	+	114	++
T-144	++	40	+
T-148	+	281	+
T-148	+	204	+
T-147	+	354	+
T-148	+	336	+
T-148	+	342	+
T-148	+/	116	+
T-148	+/	117	+
T-148	+/	280	+
T-148	+/	118	+
T-148	+/	253	+

FIG. 27A

7872-020 (SHEET 29 OF 63)

RSV	Peptide #	AVG. IC ₅₀ (XTT) ug/ml
T-22	IELSNIKE NKCNGQTDAKVVKLIKQELDKYKNAAVTELOLLMQST	>500
T-23	IELSNIKENKCNQTDAAKVKLIKQELDKY	>500
T-24	ENKCNQTDAAKVKLIKQELDKYKNAAVTELOLLMQST	>500
T-25	DAKVVKLIKQELDKYKNAAVTELOLL	>500
T-26	CNQTDAKVKLIKQELDKYKNAAVTELOLL	>500
T-27	SNIKE NKCNGTDAAKVKLIKQELDKYKNAAVTELOLL	>500
T-28	VSKQYSLALRTQWYTBVITIELSNIKEN	165
T-33A	AFIRKSGOELLHNIV	26
T-371	YTBVITIELSNIKENKUNQTDAAKVKLIKQELDKYKN	>500
T-372	YTBVITIELSNIKENKUNQTDAAKVKLIKQELDKYKN	NOT TESTED
T-373	SVITIELSNIKENKUNQTDAAKVKLIKQELDKYKN	>500
T-374	SNIKENKUNQTDAAKVKLIKQELDKYKNAAVTELOLL	>500
T-375	KIKENKUNQTDAAKVKLIKQELDKYKNAAVTELOLLMQB	>500
T-376	AVSKQYSLALRTQWYTBVITIELSNIKENKUNQTDAA	>100

7872-020 (SHEET 30 OF 63)

RSV DP-107-LIKE REGION (F1)		RSV		Position Assay		Position Assay	
RSV	DP-107	RSV	DP-107	AV	AV	Position Assay	Position Assay
T-107	T-107	T-107	T-107	204	204	204	204
T-108	T-108	T-108	T-108	159	159	159	159
T-109	T-109	T-109	T-109	159	159	159	159
T-110	T-110	T-110	T-110	159	159	159	159
T-111	T-111	T-111	T-111	159	159	159	159
T-112	T-112	T-112	T-112	159	159	159	159
T-113	T-113	T-113	T-113	159	159	159	159
T-114	T-114	T-114	T-114	159	159	159	159
T-115	T-115	T-115	T-115	159	159	159	159
T-116	T-116	T-116	T-116	159	159	159	159
T-117	T-117	T-117	T-117	159	159	159	159
T-118	T-118	T-118	T-118	159	159	159	159
T-119	T-119	T-119	T-119	159	159	159	159
T-120	T-120	T-120	T-120	159	159	159	159
T-121	T-121	T-121	T-121	159	159	159	159
T-122	T-122	T-122	T-122	159	159	159	159
T-123	T-123	T-123	T-123	159	159	159	159
T-124	T-124	T-124	T-124	159	159	159	159
T-125	T-125	T-125	T-125	159	159	159	159
T-126	T-126	T-126	T-126	159	159	159	159
T-127	T-127	T-127	T-127	159	159	159	159
T-128	T-128	T-128	T-128	159	159	159	159
T-129	T-129	T-129	T-129	159	159	159	159
T-130	T-130	T-130	T-130	159	159	159	159
T-131	T-131	T-131	T-131	159	159	159	159
T-132	T-132	T-132	T-132	159	159	159	159
T-133	T-133	T-133	T-133	159	159	159	159
T-134	T-134	T-134	T-134	159	159	159	159
T-135	T-135	T-135	T-135	159	159	159	159
T-136	T-136	T-136	T-136	159	159	159	159
T-137	T-137	T-137	T-137	159	159	159	159
T-138	T-138	T-138	T-138	159	159	159	159
T-139	T-139	T-139	T-139	159	159	159	159
T-140	T-140	T-140	T-140	159	159	159	159
T-141	T-141	T-141	T-141	159	159	159	159

FIG. 27 C

7872-020 (SHEET 31 OF 63)

RSV	Peptide #	AVG. IC ₅₀ (XTT) ug/ml
T-12	VVSLSNQVSVLTSTSKVLDLKNYIDKQLL	>500
T-13	LLSTNKA VVSLSNQVSVLTSTSKVLDLKNY	>500
T-15	LLSTNKA VVSLSNQVSVLTSTSKVLDLKNY	>500
T-19	LLSTNKA VVSLSNQVSVLTSTSKVLDLKNY	>500
T-28	AGQVAVSKVLHLEGEVNNKIKSALLSTNKA VVSLSNQV	>500
T-28	AGQVAVSKVLHLEGEVNNKIKSALLSTNKA VVSLSNQV	327
T-30	VVHLEGEVNNKIKSALLSTNKA VVSLSNQVSVLTSTSK	328
T-68	VVSLSNQVSVLTSTSKVLDLKNYIDKQLL	292
T-70	VNKKIKSALLSTNKA VVSLSNQVSVLTSTSK	349
T-66	NDDQKKLMSNNVQIVRQQSYYSIMSIIEE	>500
T-576	SIENIEIVIEFQGNRRLLLEITREFSVNAGVITPVSS	>100

FIG. 27D

7872-020 (SHEET 32 OF 63)

RSV DP-178-LIKE REGION (F1)															Fusion Assay		
RSV	T-47	F1-178	T-104	T-106	T-107	T-109	T-110	T-111	T-112	T-113	T-114	T-116	T-117	T-118	AV	Purified IC50 (log/ml) (X11)	CD
															++	37	++
															+	95	
															-	86	
															++	186	
															+++	6	
															+++	8	
															++	30	
															+++	9	
															+++	8	++
															+++	6	++
															+++	5	++
															+++	6	++
															+++	9	++
															+++	14	++
															+++	5	++
															+++	6	++

FIG. 28A

7872-020 (SHEET 33 OF 63)

RSV	Peptides	AVG. IC50 (XTT) ug/ml
T-71	P I I N F Y D P L V F P S D E F D A S I S Q V N E K I N Q S L A F I R	138
T-364	R W R Q L E D R V E E L L S K L A F I R K S D E L L H N V	NOT TESTED
T-413	O E L L H N V N A O K S T	>100
T-414	K S O E L L H N V N A O K S T	>100
T-415	I R K S O E L L H N V N A O K S T	>100
T-416	A F I R K S D E L L H N V N A O K S T	>100
T-417	F O A S I S Q V N E K I N Q S L A F I	NOT TESTED
T-462	S L A F I R K S D E L L H N V N A O K S T	>100
T-463	F D A S I S Q V N E K I N Q S L A F I R K	NOT TESTED
T-465	F D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A O K	7
T-466	F D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A	4
T-467	F D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V	4
T-468	F D A S I S Q V N E K I N Q S L A F I R K S D E L L H	5
T-469	F D A S I S Q V N E K I N Q S L A F I R K S D E L	80
T-470	F D A S I S Q V N E K I N Q S L A F I R K S D	>100
T-471	A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A O K S T	8
T-472	I S Q V N E K I N Q S L A F I R K S D E L L H N V N A O K S T	6
T-473	Q V N E K I N Q S L A F I R K S D E L L H N V N A O K S T	14
T-474	N E K I N Q S L A F I R K S D E L L H N V N A O K S T	>100
T-475	K I N Q S L A F I R K S D E L L H N V N A O K S T	>100
T-476	N Q S L A F I R K S D E L L H N V N A O K S T	>100
T-720	F D A S I S Q V N E K I N Q S L A F I R K S D E L L H N V N A O K S T	NOT TESTED

FIG. 28B

7872-020 (SHEET 34 OF 63)

HPV3 DP 107-LIKE REGION (F1)																			
</																			

7872-020 (SHEET 35 OF 63)

HPV-3 DR107-Jka Wells		AVG. IC50	
T-42	A T B A G I T A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	943,000 ug/ml	
T-43	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	853,000 ug/ml	
T-39	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	720,000 ug/ml	
T-38	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	700,000 ug/ml	
T-40	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	54,788 ug/ml	
T-44	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	225,140 ug/ml	
T-45	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	483,000 ug/ml	
T-46	A A V A L V E A K Q A R S D I E K L K E A I R D T N K A V Q S V Q S S	543,000 ug/ml	
T-582 Inactivated 164	L K E A I R D T N K A V Q S V Q S S I O N L I V A I K 8	127,854 ug/ml	

29B

7872-020 (SHEET 36 OF 63)

PIV3 DP178-LIKE REGION (F1)																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				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MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSPFRVCELSSHGDLFRFSSD

♠107x178x4♠

IQCPSTGTRENTHEGLLMVFKDNIIPYSF ♠KVRSTKIVTNILYNGWYADSVTNRHE♠

EKFSVDSY ETDQMDTIYQ CYNVVKMTKD GLTRVYVDRD GVNITVNLKP TGGLANGVRR

YASQTELYDA PGWLIWYRT RTTVNCLITD MMAKSNSPFD FFVTTTGQTV EMSPFYDGKN

KETFHERADS FHVRTNYKIV DYDNRGTNPQ GERRAFLDKG TYTLSWKLEN RTAYCPLQHW

QTFDSTIATE TGKSIHFVTD EGTSSSVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD

RYTKGQEAIT YFITSGLLL AWLPLTPRSL ATVKNLTET TPTSSPPSSP SPPAPSAARG

STPAAVLRRR RRDAGNATTP VPPTAPGKSL GTLNNPATVQ IQFAYDSLRR QINRMLGDLA

RAWCLEQKRQ NMVLRELTKI NPTTVMSSY GKAVAAKRLG DVISVSQCV VQATVTLRK

SMRVPGETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TKKMTEVCQA TSQYYFQSGN

♠107x178x4♠

EIHVYNDYHH FKTIELDGIA TLQTFISLNT ♠SLIENIDEASLELYSRDEORASNVED ♠LE♠

LVS Predicted Coiled Coil

TM Potential

GIFREYNFQAQNIAGLRKDLDNAVS* GRNQ FVDGLGELMDSLGSVG QSITN

♠P12LZIPC♠

TM Potential

TM Potential

LVSTVGGLFSSLVSGFISF FK N ♠PFGGMLILVLVAGVVILVISL♠ TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQR AAQRAAGPSV

ASRALQAARDRFPGLRRRRY HDPETAAALL GEATEF

FIG. 32

7872-020 (SHEET 40 OF 63)

MMDPNSTSED VKFTPDYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQQQ

LTAYHVSTAP TGSWFSAPQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@ ▲107x178x4▲ +Dimerization+
@KRY KNRVASRKCRK ▲EK@ Q +LLOHYREVAANKSSSENDRLRLLKQ▲

MCPSLDVD+ SI IPRTDVLHE DLLNF

FIG. 33

7872-020 (SHEET 41 OF 63)

Fusion

Peptide

FAG

♥ALLMOTIS♥

LVS Coiled-Coil

♥VVLAGAALGVATAAQITAGIALHQSMLENSQAIDNLRASLETTN

QAIEAIRQAGQEMI*LAVQGVQDYINN♥ ELIPSMNQLSCDLIGQKLGLKLLRYTT

♣P23LZIPC♣

♣P6,12LZIPC♣

♣107x178x4♣

♥ALLMOTIS♥

EILSLFGPSLRD ♣PISA ♣♥EISIQALSYALGGDINKV♣ LEKLGYSGGDL♣

♣P1,12LZIPC♣

LGILES♣ RGIKARI♥ THVDTESYFIVLSIAY ♣PTLSEIKGVTVHRLEGV♣ SY

NIGSQEWYTTVPKYVATQGYLISNFDDESSCTFMPEGTVCSQNALYPMSPLLQECL

RGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA

♣P23LZIPC♣

♣P12LZIPC♣

♥ALLMOTIS♥

LVS Coiled-Coil

DHCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGP ♣P ♥IS*LERLDVGTNLGN

♦Transmembrane Region♦

AIAKLEDAKELL♣ ESSDOI*L♣ RSMK ♦GLSSTSIVYILI♥ AVCLGGLIGIPALICCC♦ RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRS

FIG. 34

7872-020 (SHEET 42 OF 63)

Pre S1 and Pre S2

MGQNLSTSNPLGFFPDHQLDPAFRANTANPDWDFNPNKDTWPDANKVGAGAFG
 LGFTPPHGGLLGWSPQAQGILQTLPANPPPASTNRQSGRQPTPLSPPLRNTHPQAM
 QWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTASPLSSIFSRI GDPALN

Major Surface Antigen (HBs)

Fusion

Peptide

✦P12 & 23LZIPC✦

MENITSG FLG ✦PLL VLQAGFFLLTRILTI✦ PQSLDSWWTSLNFLGGTTVCLG

✦P12 & 23LZIPC✦

QNSQSPTSNHSPTSCPPTC ✦PGYRWMCLRRFIIFLLCLIFLLVLLDYQGML✦

PVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPIPSSWAFGKF

♦Transmembrane Region♦LWEWASARFSWLS ♦LLVPEVQWFVGLSPTVWLSVI♦ WMMWYWGPSL♦Transmembrane Region♦♦YSILSPFLPLLPIEFCLWVYI♦

FIG. 35

7872-020 (SHEET 43 OF 63)

Fusion ♥ALLMOTI5♥ ♠107x178x4♠
Peptide *LVS Coiled Coil
AIQLIPLFVG LGI ♥TTAVSTGAAGLGVS ♠IT *QYTKLSHQLISDV

QAISSTIQDLQDOVDSLAEVVLO* NRRGLDLLTAE♠ QGGI♥

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPFWTSFHG

FLPYVMPLLGPLLCLLLVLSFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region

RLEQEDSGGSYLTLT.....????????????????????????????????.....

FIG 36

7872-020 (SHEET 44 OF 63)

MKAQKGFTLI ELMIVVAIIG ILAAIAIPQ

♠107x178x4♠

♥ALLMOTIS♥

♠♥YQDYTARTQVTRAVSEVSALKTAAESAILEGKEIVSSA♠ T♥

PK DTQYDIGFT

♠107x178x4♠

♥ALLMOTIS♥

♠♥ESTLLDGSQKSGKSIQVTDNODGTVELVATLGKSSGS♠ AIKGAVITVSR♥

KNDGV WNCKITKTPT AWKPNYAPAN CPKS

FIG. 37

7872-020 (SHEET 45 OF 63)

MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

♠107x178x4♠

♥ALLMOTI5♥

♠♥KDNTSAGVASSSSIKGKYVKEVKVENGVVTTAT♠

MNSSNVNKEIQGKKLSLWAKRQDGSVKW♥

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

FIG. 38

7872-020 (SHEET 46 OF 63)

MKKTLLGSLI LLAFAAGNVQA DINTETSGKV TFFGKVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTITLQN

CDPTTANGTA NKANKVGLYF Y

♠107x178x4♠

♥ALLMOTIS♥

♠♥SWKNVDKENNETLKNEOTTADYATNVNI♠

QLMESNGTKAISVVGKETE♥

DF MHTNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVQSSVDFQI AYE

FIG. 39

7872-020 (SHEET 47 OF 63)

MNKKLLMNFF IVSPLLLATT ATDFTPVP

♠107x178x4♠

♥ALLMOTIS♥

♠♥LSSNOIHK TAKASTNDNIKDLLDWYSSGSDTETNS♠♥

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSPAFTKGE KV

♠107x178x4♠

♠DLNTRTKKSOHTSEGTYIHEQISGVT♠

NTEKLPTPIEL PLKVKVHVKD SPLKYG

♣P12LZIPC♣

♣PKFDKKQLAISTLDFEIRHQLTQI♣

HGLYRSSDKT GGYWKITMND GSTYQSDLSK KFEYNTEKPP

INIDEIKTIE AEIN

FIG. 40

7872-020 (SHEET 48 OF 63)

♥ALLMOTIS♥

MKKTAFILLL FIALTLTTSP L ♥VNG

♠107x178x4♠

LVS Predicted Coiled-Coil

S ♠EKSEEINEKDLRKKSELORNALSNLROIY YYNEKAITENKESDD♠

QFLENTLL♥FKG FFTGHPW

♠107x178x4♠

♠YNDLLVDLGSKDATNKYKGKKVDLYGAY♠

YGYQCAGGTPNKTACMYGGVTLHDN NRLTEKKVP INLWIDGKQTTV

♣P12LZIPC♣

♣PIDKVKTSKKEVTVQELDL♣ QARHYLHGK FGLYNSDSFGGKVQ

♣P12LZIPC♣

RGLIVF HSSEGSTVSY DLFDAQGQY ♣P DTLLRIYRDN KTINSENLHI♣

DLYLYTT

FIG. 41

7872-020 (SHEET 49 OF 63)

MKKTAFTLLL FIALTLTTSP L ♡ALLMOTIS♡
♡VNGS

♠107x178x4♠

♠EKSEEINEKDLRKKSELOGTALGNLKOIYYNEKAKTENKESHDA Q♡

FLQHTILFKG FFTDHSWYN̄D LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEKKVPINLWLDGKQNTV

♠107x178x4♠

♡ALLMOTIS♡

♣P12LZIPC♣

♣P ♡L ♠ETVKTNNKKNVTVOELDLOARRYL♣ QEKYNLYN♠

SDVFDGKVQR♡ GLIVF HTSTE

♣P23LZIPC♣

♣PSVNYDLFGAQQQYSNTLLRIYRDNKTINSENMI♣ DIYLYTS

FIG. 42

7872-020 (SHEET 50 OF 63)

MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRFRSLMPRGNEYFDRGT

♥ALLMOTI5♥

♥QMNNLYDHARGTQTGFVRYDDGYV

♠107x178x4♠

♠STSLSLRSAHLA GOYILSGYSLTIYIVI♠ ANMFNVNDVISVY♥

SP HPYEQEVSA L GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQAWRE EPWIHHAPQG

CGDSSRTITG DTCNE

♥ALLMOTI5♥

♥ETQNLSTIYLR EYQSKVKRQIFSDYQSEVDIYNRI RDEL♥

FIG. 43

7872-020 (SHEET 51 OF 63)

MMFSGFNADY EASSSRCSSA SPAGDSLSTYY HSPADSFSSM

GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWL VQPA

LVSSVAPSQT RAPHPFGVPA PSAGAYS RAG VVKTMTGGRA

LVS Predicted Coiled-Coil

QSIGRRGKVE QLSPEEEKR RIRRE *RNKMA AAK

♠ 107x178x4 ♠

♥ ALLMOTIS ♥

♥ CRNRRREL ♠ TDTLQAETDOLEDEKSALQTEIANLLKEKEKL ♥

EFILAAH R* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPESEEFT LPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARVP

DMDLSGSFYA GSSSNPSSD SLSSPTLLAL

FIG. 44

7872-020 (SHEET 52 OF 63)

SGWESYYKTEGDDEEAEEEQEENLEASGDYKYSGRDSLIFLVDASKA
 MFESQSEDELTPFDMSIQCIQSVYISKIISDRDLLAVVFGTEKDKNS
 VNFKNITYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDY
 SLSEVLWVCANLFSQVQFKMSHKRIMLFTNEDNPHGNDSAKASRAR
 TKAGDLRDTGIFLDMHLKKPGGFDISLFYRDIISIAEDED

♠107x178x4♠

♥ALLMOTIS♥

LVS Predicted Coiled-Coil

♥LRVH *FEE ♠SSKLEDLLRKVRKETRKRALSRLKLNKDIV* ISV

GIYNLVQKAL♥ KPPPIKLYRETN♠ EPVKTTRTFNTSTGGLLLPSTDKR

SQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHLRPSLFVYPE
 ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK
 IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRS
 DSFENPVLQQHFRNLEALALDLME

♣P12LZIPC♣

♣PEQAVDLTLPKVEAMNKRL♣ GSLVDEFKELVYPPDYNPEGKVTKR

KHDNEGSGSKRPKVEYSEEELKTHISKGTGKFTVPMLEACRAYGLKSG

LKKQELLEALTKHFQD

FIG. 45

7872-020 (SHEET 53 OF 63)

GGGALSPQHSAVTQGSIIKNKEGMDAKS

♠107x178x4♠

♥ALLMOTI5♥

♥♠LTAWSRTLVTFKDVEVDEFTREEWKLLDT♠ AQQIVYRNV

MLENYKNLVSLGYQLT♥ KPDVILRLEKGEEPWLVEREIHQETHPD
SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEEVWKCR
DQLDKYQENPERHLRHQLIHTGEKPYECKECGKSFSRSSHLIGHQKT
HTGEEPYECKECGKSFSWFSHLVTHQRTHTGDKLYTCNQCGKSFVH
SSRLIRHQRTHTGHKPYECPECGKSFRQSTHLILHQRTHVVRPYECN
ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSSRSHLYSHQRT
TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN
DLIKHQRIHVGAETYKCNQCGIIFSQNS

♣P23LZIPC♣

♣PFIVHQIAHTGEQFLTCNQCGTALVNTSNLIGYQTNHI♣ RENAY

FIG. 46

7872-020 (SHEET 56 OF 63)

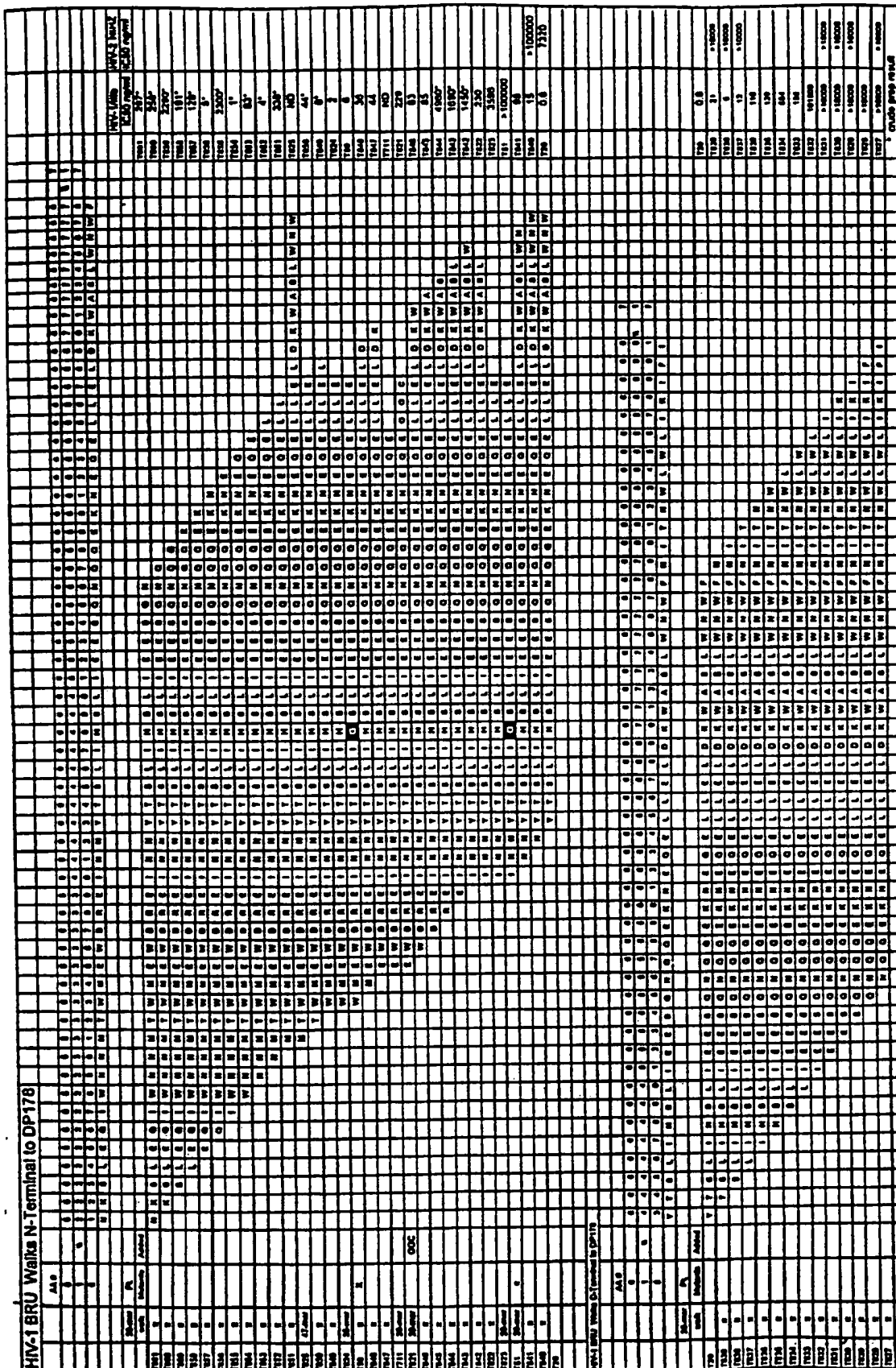


FIG. 49A

7872-020 (SHEET 57 OF 63)

HIV-1 Bru 178 Constructs, Mutations, Truncations									
Accession	Protein	Start	End	Length	Accession	Protein	Start	End	Length
14	178	1	178	178	14	178	1	178	178
7229	178	1	178	178	7229	178	1	178	178
7160	178	1	178	178	7160	178	1	178	178
7111	178	1	178	178	7111	178	1	178	178
7112	178	1	178	178	7112	178	1	178	178
7113	178	1	178	178	7113	178	1	178	178
7114	178	1	178	178	7114	178	1	178	178
7115	178	1	178	178	7115	178	1	178	178
7116	178	1	178	178	7116	178	1	178	178
7117	178	1	178	178	7117	178	1	178	178
7118	178	1	178	178	7118	178	1	178	178
7119	178	1	178	178	7119	178	1	178	178
7120	178	1	178	178	7120	178	1	178	178
7121	178	1	178	178	7121	178	1	178	178
7122	178	1	178	178	7122	178	1	178	178
7123	178	1	178	178	7123	178	1	178	178
7124	178	1	178	178	7124	178	1	178	178
7125	178	1	178	178	7125	178	1	178	178
7126	178	1	178	178	7126	178	1	178	178
7127	178	1	178	178	7127	178	1	178	178
7128	178	1	178	178	7128	178	1	178	178
7129	178	1	178	178	7129	178	1	178	178
7130	178	1	178	178	7130	178	1	178	178
7131	178	1	178	178	7131	178	1	178	178
7132	178	1	178	178	7132	178	1	178	178
7133	178	1	178	178	7133	178	1	178	178
7134	178	1	178	178	7134	178	1	178	178
7135	178	1	178	178	7135	178	1	178	178
7136	178	1	178	178	7136	178	1	178	178
7137	178	1	178	178	7137	178	1	178	178
7138	178	1	178	178	7138	178	1	178	178
7139	178	1	178	178	7139	178	1	178	178
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7141	178	1	178	178	7141	178	1	178	178
7142	178	1	178	178	7142	178	1	178	178
7143	178	1	178	178	7143	178	1	178	178
7144	178	1	178	178	7144	178	1	178	178
7145	178	1	178	178	7145	178	1	178	178
7146	178	1	178	178	7146	178	1	178	178
7147	178	1	178	178	7147	178	1	178	178
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7150	178	1	178	178	7150	178	1	178	178
7151	178	1	178	178	7151	178	1	178	178
7152	178	1	178	178	7152	178	1	178	178
7153	178	1	178	178	7153	178	1	178	178
7154	178	1	178	178	7154	178	1	178	178
7155	178	1	178	178	7155	178	1	178	178
7156	178	1	178	178	7156	178	1	178	178
7157	178	1	178	178	7157	178	1	178	178
7158	178	1	178	178	7158	178	1	178	178
7159	178	1	178	178	7159	178	1	178	178
7160	178	1	178	178	7160	178	1	178	178
7161	178	1	178	178	7161	178	1	178	178
7162	178	1	178	178	7162	178	1	178	178
7163	178	1	178	178	7163	178	1	178	178
7164	178	1	178	178	7164	178	1	178	178
7165	178	1	178	178	7165	178	1	178	178
7166	178	1	178	178	7166	178	1	178	178
7167	178	1	178	178	7167	178	1	178	178
7168	178	1	178	178	7168	178	1	178	178
7169	178	1	178	178	7169	178	1	178	178
7170	178	1	178	178	7170	178	1	178	178
7171	178	1	178	178	7171	178	1	178	178
7172	178	1	178	178	7172	178	1	178	178
7173	178	1	178	178	7173	178	1	178	178
7174	178	1	178	178	7174	178	1	178	178
7175	178	1	178	178	7175	178	1	178	178
7176	178	1	178	178	7176	178	1	178	178
7177	178	1	178	178	7177	178	1	178	178
7178	178	1	178	178	7178	178	1	178	178
7179	178	1	178	178	7179	178	1	178	178
7180	178	1	178	178	7180	178	1	178	178
7181	178	1	178	178	7181	178	1	178	178
7182	178	1	178	178	7182	178	1	178	178
7183	178	1	178	178	7183	178	1	178	178
7184	178	1	178	178	7184	178	1	178	178
7185	178	1	178	178	7185	178	1	178	178
7186	178	1	178	178	7186	178	1	178	178
7187	178	1	178	178	7187	178	1	178	178
7188	178	1	178	178	7188	178	1	178	178
7189	178	1	178	178	7189	178	1	178	178
7190	178	1	178	178	7190	178	1	178	178
7191	178	1	178	178	7191	178	1	178	178
7192	178	1	178	178	7192	178	1	178	178
7193	178	1	178	178	7193	178	1	178	178
7194	178	1	178	178	7194	178	1	178	178
7195	178	1	178	178	7195	178	1	178	178
7196	178	1	178	178	7196	178	1	178	178
7197	178	1	178	178	7197	178	1	178	178
7198	178	1	178	178	7198	178	1	178	178
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7200	178	1	178	178	7200	178	1	178	178
7201	178	1	178	178	7201	178	1	178	178
7202	178	1	178	178	7202	178	1	178	178
7203	178	1	178	178	7203	178	1	178	178
7204	178	1	178	178	7204	178	1	178	178
7205	178	1	178	178	7205	178	1	178	178
7206	178	1	178	178	7206	178	1	178	178
7207	178	1	178	178	7207	178	1	178	178
7208	178	1	178	178	7208	178	1	178	178
7209	178	1	178	178	7209	178	1	178	178
7210	178	1	178	178	7210	178	1	178	178
7211	178	1	178	178	7211	178	1	178	178
7212	178	1	178	178	7212	178	1	178	178
7213	178	1	178	178	7213	178	1	178	178
7214	178	1	178	178	7214	178	1	178	178
7215	178	1	178	178	7215	178	1	178	178
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7218	178	1	178	178	7218	178	1	178	178
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7223	178	1	178	178	7223	178	1	178	178
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7227	178	1	178	178	7227	178	1	178	178
7228	178	1	178	178	7228	178	1	178	178
7229	178	1	178	178	7229	178	1	178	178
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7231	178	1	178	178	7231	178	1	178	178
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7235	178	1	178	178	7235	178	1	178	178
7236	178	1	178	178	7236	178	1	178	178
7237	178	1	178	178	7237	178	1	178	178
7238	178	1	178	178	7238	178	1	178	178
7239	178	1	178	178	7239	178	1	178	178
7240	178	1	178	178	7240	178	1	178	178
7241	178	1	178	178	7241	178	1	178	178
7242	178	1	178	178	7242	178	1	178	178
7243	178	1	178	178	7243	178	1	178	178
7244	178	1	178	178	7244	178	1	178	178
7245	178	1	178	178	7245	178	1	178	178
7246	178	1	178	178	7246	178	1	178	178
7247	178	1	178	178	7247	178	1	178	178
7248	178	1	178	178	7248	178	1	178	178
7249	178	1	178	178	7249	178	1	178	178
7250	178	1	178	178	7250	178	1	178	178
7251	178	1	178	178	7251	178	1	178	178
7252	178	1	178	178	7252	178	1	178	178
7253	178	1	178	178	7253	178	1	178	178
7254	178	1	178	178	7254	178	1	178	178
7255	178	1	178	178	7255	178	1	178	178
7256	178	1	178	178	7256	178	1	178	178
7257	178	1	178	178	7257	178	1	178</	

F. L. 493

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HIV-1 Env 178 Constructs, Mutations																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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FIG. 49C

7872-020 (SHEET 59 OF 63)

HIV-1 BRU DP-107 peptides																			
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120
121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140
141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160
161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180
181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200
201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220
221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240
241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260
261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280
281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320
321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340
341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360
361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380
381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400
401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420
421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440
441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460
461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480
481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500
501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520
521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540
541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560
561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580
581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600
601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620
621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640
641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660
661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680
681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700
701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720
721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740
741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760
761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780
781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800
801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820
821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840
841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860
861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880
881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900
901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920
921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940
941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960
961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980
981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000

FIG. 50

51A

EPSTEIN-BARR VIRUS STRAIN B95-8 BZLF1 TRANSACTIVATOR PROTEIN EB1 OR ZEBRA																														ACT										Rat														
Readline	173	B	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	219							
T421	173	B	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	208						
T422	174	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	209							
T423	175	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	210							
T424	176	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	211							
T425	177	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	212							
T426	178	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	213							
T427	179	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	214							
T428	180	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	215							
T429	181	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	216							
T430	182	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	217							
T431	183	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	218							
T432	184	E	L	E	I	K	R	Y	K	N	R	V	A	B	R	K	C	R	A	K	F	K	Q	L	Q	H	Y	R	E	V	A	A	A	A	K	B	B	E	N	D	R	L	R	L	L	L	219							
T433																																																		219				
T434																																																		219				
																					</																																	

7872-020 (SHEET 61 OF 63)

Residue	197	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		242		46
T-447	197	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		232		36
T-448	198	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		233		36
T-449	199	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		234		36
T-450	200	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		235		36
T-451	201	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		236		36
T-452	202	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		237		36
T-453	203	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		238		36
T-454	204	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		239		36
T-455	205	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		240		36
T-456	206	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		241		36
T-457	207	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		242		36
T-458	208	L	Q	H	Y	R	E	V	A	A	A	K	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D		243		36

Residue	200	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F		246		37
T-459	209	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F		244		36
T-460	210	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F		245		36
T-461	211	S	E	N	D	R	L	R	L	L	K	Q	M	C	P	S	L	D	V	D	S	I	I	P	R	T	P	D	V	L	H	E	D	L	L	N	F		246		36

FIG. 51B

7872-020 (SHEET 62 OF 63)

Domain I:

174P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-S-P220

P-L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T
L-L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T
L-V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V
V-L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C
L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L
Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G
A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q
G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N
F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S
F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q
L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-S

I=16. 52A

7872-020 (SHEET 63 OF 63)

Domain II:
223P.G.Y.R.W.M.C.L.R.F.I.F.L.L.L.C.L.I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.G.S.S.T.S.T.G.P.C.R.T.C.M.T.T281

P.O.Y.R.W.M.C.L.R.R.F.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L
G.Y.R.W.M.C.L.R.R.P.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P
Y.R.W.M.C.L.R.R.F.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V
R.W.M.C.L.R.R.F.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C
W.N.C.L.R.R.F.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P
N.C.L.R.R.F.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L
C.L.R.R.F.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I
L.R.R.R.F.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O
R.R.R.F.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S
R.F.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S
P.I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T
I.I.F.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T
I.F.L.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S
P.L.F.I.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T
L.F.I.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O
F.I.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P
I.L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C
L.L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R
L.L.C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R.T
L.L.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R.T.C
C.L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R.T.C.M
L.I.P.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R.T.C.M.T
I.F.L.L.V.L.L.D.Y.Q.G.M.L.P.V.C.P.L.I.P.O.S.S.T.S.T.O.P.C.R.T.C.M.T.T

P-26. 52 B

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/16733**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : C07K 7/04, 14/025, 14/16; C12N 9/94, 9/96, 9/98, 9/99

US CL : 530/324; 424/184.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 530/324, 325, 326, 327, 328, 329; 424/184.1, 185.1, 186.1, 187.1, 188.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

MEDLINE, AIDSLINE, APS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ----- Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 89, Number 21, issued November 1992, Wild et al, "A Synthetic Peptide Inhibitor of Human Immunodeficiency Virus Replication: Correlation Between Solution Structure and Viral Inhibition", pages 10537-41, see entire document.	1-3, 9, and 10 ----- 4-8 and 11-15

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"A" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

28 MARCH 1996

Date of mailing of the international search report

09 APR 1996

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/16733

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ----- Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 91, Number 26, issued December 1994, Wild et al, "Propensity for a Leucine Zipper-Like Domain of Human Immunodeficiency Virus Type 1 gp41 to Form Oligomers Correlates With a Role in Virus-Induced Fusion Rather Than Assembly of the Glycoprotein Complex", pages 12676-80, see entire document.	1-3, 9 and 10 ----- 4-8 and 11-15
X ----- Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 81, Number 24, issued December 1984, Collins et al, "Nucleotide Sequence of the Gene Encoding the Fusion (F) Glycoprotein of Human Respiratory Syncytial Virus", pages 7683-87, see pages 7683 and 7685.	1 and 4 ----- 9 and 11
X ----- Y	VIROLOGY, Volume 204, Number 2, issued 01 November 1994, Bousse et al, "Regions on the Hemagglutinin-Neuraminidase Proteins of Human Parainfluenza Virus Type-1 and Sendai Virus Important for Membrane Fusion", pages 506-514, see pages 506 and 510-513.	1 and 5 ----- 9 and 12
X ----- Y	JOURNAL OF VIROLOGY, Volume 67, Number 9, issued September 1993, Wang et al, "Ion Channel Activity of Influenza A Virus M2 Protein: Characterization of the Amantidine Block", pages 5585-94, see pages 5585-86.	1 and 6 ----- 9 and 13
X ----- Y	JOURNAL OF VIROLOGY, Volume 67, Number 5, issued May 1993, Lazinski et al, "Relating Structure to Function in the Hepatitis Delta Virus Antigen", pages 2672-80, see pages 2672-73 and 2678.	1 and 7 ----- 9 and 14
P, Y	JOURNAL OF EXPERIMENTAL MEDICINE, Volume 182, Number 2, issued August 1995, Suzuki et al, "Viral Interleukin 10 (IL-10), the Human Herpes Virus 4 Cellular IL-10 Homologue, Induces Local Anergy to Allogenic and Syngeneic Tumors", pages 477-486, see entire document.	1, 8, 9, and 15